

Protein Sequence Searches - February 2005

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OM protein - protein search, using SW model

Run on: July 19, 2005, 23:49:42 ; Search time 22 Seconds
(without alignments)
756.670 Million cell updates/sec

Title: US-10-036-214-61

Perfect score: 1204
Sequence: 1 MGMTMLVTALLGLMMVV.....PTLQAPRGASPEPKTROR 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1181	98.1	227	3 US-09-208-718-3	Sequence 3, Appli
2	1177	97.8	227	4 US-09-621-976-8	Sequence 8, Appli
3	1177	97.8	227	4 US-09-513-999C-8	Sequence 8, Appli
4	1177	97.8	227	4 US-09-471-276-8	Sequence 8, Appli
5	235.5	19.6	187	4 US-09-497-308A-7	Sequence 7, Appli
6	231	19.2	152	3 US-09-208-718-6	Sequence 6, Appli
7	218.5	18.1	186	4 US-09-492-308A-8	Sequence 8, Appli
8	210.5	17.5	187	1 US-08-403-378B-4	Sequence 4, Appli
9	205	17.0	187	1 US-08-403-378B-15	Sequence 15, Appli
10	164	13.6	175	3 US-09-060-726A-2	Sequence 2, Appli
11	164	13.6	175	4 US-09-845-849A-2	Sequence 2, Appli
12	161.5	13.4	141	4 US-09-270-767-4392C	Sequence 4392C, A
13	157	13.0	174	4 US-09-248-796A-16385	Sequence 16385, A
14	148	12.3	181	4 US-09-492-308A-2	Sequence 2, Appli
15	142.5	11.8	177	4 US-09-492-308A-23	Sequence 23, Appli
16	139	11.5	152	1 US-07-644-372-2	Sequence 2, Appli
17	137.5	11.4	120	4 US-09-270-767-33653	Sequence 33653, A
18	137.5	11.4	120	4 US-09-270-767-48870	Sequence 48870, A
19	137.5	11.4	177	4 US-09-492-308A-5	Sequence 5, Appli
20	137.5	11.4	177	4 US-09-492-308A-22	Sequence 22, Appli
21	131.5	10.9	177	4 US-09-492-308A-21	Sequence 21, Appli
22	130.5	10.8	177	4 US-09-492-308A-20	Sequence 20, Appli
23	102.5	8.5	115	4 US-09-845-849A-8	Sequence 8, Appli
24	99.5	8.3	132	4 US-09-270-767-57507	Sequence 57507, A
25	99.5	8.3	268	4 US-09-270-767-42230	Sequence 42230, A
26	98.5	8.2	172	4 US-09-902-540-12693	Sequence 12693, A
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32	89.5	7.4	176	4 US-09-050-739-50	Sequence 50, Appli
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35	87	7.2	165	4 US-09-302-331B-12	Sequence 12, Appli
36	85	7.1	155	4 US-09-902-331B-14	Sequence 14, Appli
37	83	6.9	591	4 US-09-949-016-11666	Sequence 11666, A
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59	74	6.1	233	3 US-08-437-642B-25	Sequence 25, Appli
60	74	6.1	233	4 US-08-146-206C-25	Sequence 25, Appli
61	74	6.1	233	4 US-09-705-686-25	Sequence 25, Appli
62	74	6.1	233	4 US-09-705-392A-25	Sequence 25, Appli
63	74	6.1	233	4 US-09-705-398A-25	Sequence 25, Appli
64	74	6.1	233	5 PCT-US93-078332-25	Sequence 25, Appli
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66	73.5	6.1	212	2 US-09-102-593-3	Sequence 3, Appli
67	73.5	6.1	212	3 US-09-293-724-3	Sequence 3, Appli
68	73.5	6.1	244	4 US-09-328-352-6433	Sequence 6433, Ap
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71	73	6.1	1711	2 US-08-342-930-2	Sequence 2, Appli
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73	72.5	6.0	327	4 US-09-385-219A-58	Sequence 58, Appli
74	72.5	6.0	1102	2 US-08-916-917-4	Sequence 4, Appli
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80	72.5	6.0	1193	4 US-09-227-725A-4	Sequence 4, Appli
81	72.5	6.0	1211	4 US-09-167-206-14	Sequence 14, Appli
82	72	6.0	210	3 US-09-160-221A-2	Sequence 2, Appli
83	72	6.0	336	4 US-09-252-991A-22158	Sequence 22158, A
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85	71.5	5.9	575	3 US-08-922-865-2	Sequence 2, Appli
86	71.5	5.9	575	4 US-09-510-849-2	Sequence 2, Appli
87	71.5	5.9	1114	2 US-08-576-626A-31	Sequence 31, Appli
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92	71	5.9	1935	4 US-09-949-016-10970	Sequence 10970, A
93	70.5	5.9	71	4 US-09-492-308A-15	Sequence 15, Appli
94	70.5	5.9	334	4 US-09-489-039A-8445	Sequence 8445, Ap
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96	70	5.8	491	4 US-09-248-796A-14421	Sequence 14421, A
97	69.5	5.8	192	4 US-09-248-796A-15447	Sequence 15447, A
98	69.5	5.8	438	4 US-08-462-934A-12	Sequence 12, Appli
99	69.5	5.8	681	4 US-09-252-991A-25690	Sequence 25690, A
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102	69	5.7	212	3	US-09-103-079-21	Sequence 21, Appl	175	67	5.6	568	4	US-08-813-323C-2	Sequence 2, Appl1
103	69	5.7	212	4	US-09-425-021-21	Sequence 21, Appl	176	67	5.6	640	4	US-09-949-016-7992	Sequence 7992, Ap
104	69	5.7	212	4	US-09-564-829-15	Sequence 15, Appl	177	67	5.6	812	1	US-08-446-794A-4	Sequence 4, Appl1
105	69	5.7	214	1	US-08-458-516-12	Sequence 12, Appl	178	66.5	5.5	269	4	US-09-531-056A-14	Sequence 14, Appl
106	69	5.7	214	2	US-07-934-373C-39	Sequence 39, Appl	179	66.5	5.5	285	3	US-09-289-349-12	Sequence 12, Appl
107	69	5.7	214	3	US-08-437-642B-39	Sequence 39, Appl	180	66.5	5.5	328	4	US-09-531-056A-13	Sequence 13, Appl
108	69	5.7	214	5	PCT-US93-07832-39	Sequence 39, Appl	181	66.5	5.5	331	4	US-09-531-056A-12	Sequence 11, Appl
109	69	5.7	763	4	US-09-543-681A-5099	Sequence 5099, Ap	182	66.5	5.5	398	4	US-09-489-039A-10213	Sequence 10213, A
110	69	5.7	773	4	US-09-585-858-35	Sequence 35, Appl	183	66.5	5.5	451	3	US-08-878-177-2	Sequence 2, Appl1
111	69	5.7	773	4	US-10-270-878-35	Sequence 35, Appl	184	66.5	5.5	477	4	US-09-902-540-12529	Sequence 12529, A
112	69	5.7	1064	4	US-09-626-301-4	Sequence 35, Appl	185	66.5	5.5	514	4	US-09-252-991A-28208	Sequence 28208, A
113	68.5	5.7	343	4	US-09-360-376-17	Sequence 17, Appl	186	66.5	5.5	660	4	US-09-252-991A-32206	Sequence 32206, A
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117	68.5	5.7	605	4	US-09-833-616-2	Sequence 2, Appl1	190	66	5.5	277	4	US-09-107-532A-7213	Sequence 7213, Ap
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119	68	5.6	214	3	US-08-811-757-1	Sequence 1, Appl1	192	66	5.5	462	4	US-09-252-991A-18530	Sequence 18530, A
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121	68	5.6	229	3	US-09-045-973-7	Sequence 7, Appl1	194	66	5.5	735	4	US-09-902-540-13533	Sequence 13533, A
122	68	5.6	233	4	US-08-030-175-43	Sequence 43, Appl	195	66	5.5	738	4	US-09-949-016-9808	Sequence 9808, Ap
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131	67.5	5.6	472	1	US-09-088-641-4	Sequence 4, Appl1	204	65.5	5.4	279	3	US-09-318-793A-5	Sequence 5, Appl1
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134	67.5	5.6	512	3	US-08-951-742-4	Sequence 4, Appl1	207	65.5	5.4	382	4	US-09-402-532-4	Sequence 4, Appl1
135	67.5	5.6	596	6	US-08-481-190-8	Sequence 8, Appl1	208	65.5	5.4	401	4	US-09-864-894C-1	Sequence 1, Appl1
136	67.5	5.6	596	5	PCT-US93-00869-8	Sequence 8, Appl1	209	65.5	5.4	426	4	US-09-902-540-12700	Sequence 12700, A
137	67.5	5.6	610	4	US-09-248-796A-17030	Sequence 17030, A	210	65.5	5.4	427	4	US-10-179-784-3	Sequence 3, Appl1
138	67.5	5.6	921	3	US-09-514-599-2	Sequence 2, Appl1	211	65.5	5.4	454	4	US-09-252-991A-28716	Sequence 28716, A
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141	67	5.6	153	4	US-08-813-323C-11	Sequence 11, Appl	214	65.5	5.4	586	4	US-09-691-344A-4	Sequence 4, Appl1
142	67	5.6	158	3	US-08-411-768B-5	Sequence 5, Appl1	215	65.5	5.4	587	4	US-09-107-532A-6405	Sequence 6405, Ap
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164	67	5.6	468	4	US-09-268-544B-36	Sequence 36, Appl	237	65	5.4	1434	4	US-08-918-658-10	Sequence 10, Appl
165	67	5.6	465	4	US-09-720-318A-12	Sequence 12, Appl	238	65	5.4	1434	4	US-09-724-631-10	Sequence 10, Appl
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169	67	5.6	556	3	US-08-798-269-1	Sequence 1, Appl1	242	65	5.4	1447	3	US-08-656-055-19	Sequence 19, Appl
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172	67	5.6	567	4	US-09-645-926A-7	Sequence 7, Appl1	245	65	5.4	1447	3	US-08-918-658-19	Sequence 19, Appl
173	67	5.6	567	4	US-08-813-323C-1	Sequence 1, Appl1	246	65	5.4	1447	4	US-09-724-631-19	Sequence 19, Appl

247	65	5.4	1447	4	US-08-954-701A-19	Sequence 19, Appl	320	63.5	5.3	394	4	US-09-252-991A-32042	Sequence 32042, A
248	65	5.4	1447	5	PCT-US95-13333-19	Sequence 19, Appl	321	63.5	5.3	414	4	US-09-949-016-6906	Sequence 6906, Ap
249	64.5	5.4	108	4	US-09-513-999C-4705	Sequence 4705, Ap	322	63.5	5.3	431	4	US-09-252-991A-28694	Sequence 28694, A
250	64.5	5.4	223	4	US-09-270-767-38681	Sequence 38681, A	323	63.5	5.3	501	1	US-08-149-105-17	Sequence 17, Appl
251	64.5	5.4	223	4	US-09-270-767-38688	Sequence 53898, A	324	63.5	5.3	501	1	US-08-317-847-17	Sequence 17, Appl
252	64.5	5.4	265	4	US-09-710-279-174	Sequence 174, App	325	63.5	5.3	501	1	US-09-949-016-9766	Sequence 9766, Ap
253	64.5	5.4	300	4	US-09-585-858-45	Sequence 45, Appl	326	63.5	5.3	503	3	US-09-382-256-10	Sequence 10, Appl
254	64.5	5.4	300	4	US-10-270-878-45	Sequence 45, Appl	327	63.5	5.3	503	3	US-09-395-115-10	Sequence 10, Appl
255	64.5	5.4	322	4	US-09-640-211A-784	Sequence 784, App	328	63.5	5.3	503	3	US-08-123-934A-10	Sequence 10, Appl
256	64.5	5.4	360	4	US-09-252-991A-21624	Sequence 21624, A	329	63.5	5.3	503	3	US-08-436-265-10	Sequence 10, Appl
257	64.5	5.4	369	4	US-09-328-352-4297	Sequence 4297, Ap	330	63.5	5.3	503	3	US-09-679-187-10	Sequence 10, Appl
258	64.5	5.4	437	3	US-09-134-001C-5342	Sequence 5342, Ap	331	63.5	5.3	503	4	US-09-874-628-10	Sequence 10, Appl
259	64.5	5.4	501	3	US-09-367-206-3	Sequence 3, Appl	332	63.5	5.3	503	4	US-09-267-9630-10	Sequence 10, Appl
260	64.5	5.4	533	4	US-09-489-039A-7511	Sequence 7511, Ap	333	63.5	5.3	503	4	US-09-949-016-6528	Sequence 6528, Ap
261	64.5	5.4	550	4	US-09-344-510B-4	Sequence 4, Appl	334	63.5	5.3	503	5	PCT-US94-10080-10	Sequence 10, Appl
262	64.5	5.4	554	4	US-09-438-185A-124	Sequence 124, App	335	63.5	5.3	518	4	US-09-248-796A-18577	Sequence 18577, A
263	64.5	5.4	708	4	US-09-902-540-14001	Sequence 14001, A	336	63.5	5.3	636	4	US-09-489-039A-13547	Sequence 13547, A
264	64.5	5.4	707	1	US-08-803-973-12	Sequence 12, Appl	337	63.5	5.3	674	1	US-08-803-973-7	Sequence 7, Appl
265	64.5	5.4	707	1	US-08-803-972-12	Sequence 12, Appl	338	63.5	5.3	731	4	US-08-803-972-7	Sequence 7, Appl
266	64.5	5.4	812	1	US-08-446-794A-2	Sequence 2, Appl	339	63.5	5.3	731	4	US-09-248-796A-19041	Sequence 19041, A
267	64.5	5.4	812	1	US-08-750-007-3	Sequence 3, Appl	340	63.5	5.3	786	4	US-09-543-681A-6650	Sequence 6650, Ap
268	64.5	5.4	812	2	US-08-945-024-2	Sequence 2, Appl	341	63.5	5.3	899	4	US-09-107-433-3196	Sequence 3196, Ap
269	64.5	5.4	834	2	US-09-252-991A-28145	Sequence 28145, A	342	63.5	5.3	1266	6	5206163-1	Patent No. 5206163
270	64.5	5.4	845	4	US-09-949-016-8331	Sequence 8331, Ap	343	63.5	5.3	1266	6	5206163-1	Patent No. 5206163
271	64.5	5.4	1014	4	US-09-344-510B-3	Sequence 3, Appl	344	63.5	5.3	1399	4	US-09-388-221B-4	Sequence 4, Appl
272	64.5	5.4	1172	4	US-09-328-352-6071	Sequence 6071, Ap	345	63.5	5.3	1433	4	US-09-388-221B-6	Sequence 6, Appl
273	64	5.3	212	4	US-10-011-125A-5	Sequence 5, Appl	346	63.5	5.3	1456	1	US-08-803-973-2	Sequence 2, Appl
274	64	5.3	214	2	US-07-934-373C-40	Sequence 40, Appl	347	63.5	5.3	1456	1	US-08-803-972-2	Sequence 2, Appl
275	64	5.3	214	2	US-08-788-800-11	Sequence 11, Appl	348	63.5	5.3	1473	4	US-09-388-221B-2	Sequence 2, Appl
276	64	5.3	214	3	US-08-437-642B-40	Sequence 40, Appl	349	63.5	5.3	2637	2	US-08-751-189-3	Sequence 3, Appl
277	64	5.3	214	3	US-09-097-309-2	Sequence 2, Appl	350	63.5	5.3	2637	2	US-09-060-836-3	Sequence 3, Appl
278	64	5.3	214	3	US-09-097-171A-2	Sequence 2, Appl	351	63.5	5.3	2637	2	US-09-184-445-3	Sequence 3, Appl
279	64	5.3	214	3	US-09-460-587-2	Sequence 2, Appl	352	63	5.2	113	4	US-09-621-976-4206	Sequence 406, Ap
280	64	5.3	214	4	US-09-940-166A-2	Sequence 2, Appl	353	63	5.2	206	1	US-08-097-827-7	Sequence 7, Appl
281	64	5.3	214	5	PCT-US93-07832-40	Sequence 40, Appl	354	63	5.2	206	1	US-08-494-574-7	Sequence 7, Appl
282	64	5.3	215	4	US-09-902-540-10404	Sequence 10404, A	355	63	5.2	229	4	US-09-543-681A-7402	Sequence 7402, Ap
283	64	5.3	216	2	US-08-821-637-3	Sequence 3, Appl	356	63	5.2	233	3	US-09-512-342-14	Sequence 14, Appl
284	64	5.3	216	3	US-09-215-160-3	Sequence 3, Appl	357	63	5.2	301	4	US-09-107-532A-4953	Sequence 4953, Ap
285	64	5.3	237	3	US-09-460-587-6	Sequence 6, Appl	358	63	5.2	336	4	US-09-489-039A-13630	Sequence 13630, A
286	64	5.3	237	3	US-09-097-309-6	Sequence 6, Appl	359	63	5.2	407	4	US-09-489-039A-13630	Sequence 13630, A
287	64	5.3	237	3	US-09-097-171A-10	Sequence 10, Appl	360	63	5.2	416	4	US-09-949-016-8237	Sequence 8237, Ap
288	64	5.3	237	3	US-09-422-712B-2	Sequence 2, Appl	361	63	5.2	419	4	US-09-949-016-8237	Sequence 8237, Ap
289	64	5.3	237	3	US-09-607-756-2	Sequence 2, Appl	362	63	5.2	438	1	US-09-252-991A-22888	Sequence 22888, A
290	64	5.3	237	4	US-09-460-587-6	Sequence 6, Appl	363	63	5.2	438	1	US-08-097-827-11	Sequence 11, Appl
291	64	5.3	264	4	US-09-940-166A-6	Sequence 6, Appl	364	63	5.2	478	3	US-08-494-574-11	Sequence 11, Appl
292	64	5.3	295	3	US-09-710-279-286	Sequence 286, App	365	63	5.2	478	3	US-08-878-177-4	Sequence 4, Appl
293	64	5.3	296	4	US-09-134-001C-4466	Sequence 4466, Ap	366	63	5.2	483	4	US-09-902-540-12728	Sequence 12728, A
294	64	5.3	337	3	US-09-902-540-14033	Sequence 14033, A	367	63	5.2	485	3	US-09-651-941-9	Sequence 9, Appl
295	64	5.3	337	4	US-09-331-581-24	Sequence 24, Appl	368	63	5.2	485	4	US-09-955-597-9	Sequence 9, Appl
296	64	5.3	421	4	US-09-949-016-7799	Sequence 7799, Ap	369	63	5.2	488	4	US-09-786-240-1	Sequence 1, Appl
297	64	5.3	429	4	US-09-198-452A-535	Sequence 535, App	370	63	5.2	508	3	US-09-655-270A-9	Sequence 9, Appl
298	64	5.3	449	4	US-09-438-185A-497	Sequence 497, App	371	63	5.2	546	2	US-08-904-871-5	Sequence 5, Appl
299	64	5.3	449	4	US-09-198-452A-1114	Sequence 1114, App	372	63	5.2	559	4	US-08-492-027A-8	Sequence 8, Appl
300	64	5.3	464	4	US-09-438-185A-1040	Sequence 1040, Ap	373	63	5.2	559	4	US-09-832-441-2	Sequence 2, Appl
301	64	5.3	532	1	US-09-438-185A-1040	Sequence 1040, Ap	374	63	5.2	559	4	US-09-832-441-2	Sequence 2, Appl
302	64	5.3	532	2	US-09-579-777A-2	Sequence 2, Appl	375	63	5.2	622	3	US-09-833-102-2	Sequence 2, Appl
303	64	5.3	555	1	US-08-579-777A-2	Sequence 2, Appl	376	63	5.2	725	4	US-09-305-381-2	Sequence 2, Appl
304	64	5.3	555	2	US-08-440-377A-6	Sequence 6, Appl	377	63	5.2	725	4	US-09-252-991A-23752	Sequence 23752, A
305	64	5.3	768	2	US-08-687-852-6	Sequence 6, Appl	378	63	5.2	768	3	US-08-904-871-6	Sequence 6, Appl
306	64	5.3	778	2	US-09-540-236-2782	Sequence 2782, Ap	379	63	5.2	812	4	US-08-304-871-13	Sequence 13, Appl
307	64	5.3	857	4	US-09-906-925-4	Sequence 9, Appl	380	63	5.2	812	4	US-09-489-039A-12075	Sequence 12075, A
308	63.5	5.3	1069	4	US-09-252-991A-31764	Sequence 31764, A	381	63	5.2	812	4	US-09-489-039A-12075	Sequence 12075, A
309	63.5	5.3	230	4	US-09-902-540-11566	Sequence 11566, A	382	63	5.2	812	4	US-08-220-151-3	Sequence 3, Appl
310	63.5	5.3	235	3	US-09-248-796A-18983	Sequence 18983, A	383	63	5.2	812	4	US-08-220-151-3	Sequence 3, Appl
311	63.5	5.3	235	3	US-09-423-439-18	Sequence 18, Appl	384	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
312	63.5	5.3	239	3	US-09-004-721-44	Sequence 44, Appl	385	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
313	63.5	5.3	239	3	US-08-749-659-44	Sequence 44, Appl	386	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
314	63.5	5.3	242	3	US-09-004-721-41	Sequence 41, Appl	387	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
315	63.5	5.3	242	3	US-09-032-215-47	Sequence 47, Appl	388	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
316	63.5	5.3	242	3	US-09-032-215-47	Sequence 47, Appl	389	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
317	63.5	5.3	242	3	US-08-749-659-41	Sequence 41, Appl	390	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
318	63.5	5.3	300	4	US-08-749-659-41	Sequence 41, Appl	391	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
319	63.5	5.3	314	4	US-08-158-735A-17	Sequence 17, Appl	392	63	5.2	812	4	US-08-413-118-3	Sequence 3, Appl
			358	3	US-09-360-376-14	Sequence 14, Appl							
					US-09-821-736-4	Sequence 4, Appl							

333	63	5.2	1085	3	US-08-484-159-5	Sequence 5, Appli	466	61.5	5.1	414	4	US-09-248-796A-19046	Sequence 19046, A
334	63	5.2	1151	4	US-09-710-279-2448	Sequence 2448, Ap	467	61.5	5.1	457	3	US-08-431-517F-14	Sequence 14, Appli
335	63	5.2	1154	4	US-09-134-001C-3428	Sequence 3428, Ap	468	61.5	5.1	472	1	US-08-749-903-5	Sequence 5, Appli
336	63	5.2	1481	3	US-09-251-645-14	Sequence 14, Appli	469	61.5	5.1	472	3	US-09-088-641-1	Sequence 5, Appli
337	62.5	5.2	134	4	US-09-252-991A-25154	Sequence 25154, A	470	61.5	5.1	483	3	US-08-431-517F-13	Sequence 13, Appli
338	62.5	5.2	214	2	US-08-480-753-6	Sequence 6, Appli	471	61.5	5.1	569	4	US-09-514-245-22	Sequence 22, Appli
339	62.5	5.2	214	2	US-09-041-889-11	Sequence 11, Appli	472	61.5	5.1	612	4	US-09-248-796A-15682	Sequence 15682, A
340	62.5	5.2	214	3	US-08-837-058-11	Sequence 11, Appli	473	61.5	5.1	617	4	US-09-252-991A-29507	Sequence 29507, A
401	62.5	5.2	210	4	US-09-417-264-11	Sequence 11, Appli	474	61.5	5.1	727	4	US-09-585-858-32	Sequence 32, Appli
402	62.5	5.2	220	4	US-09-134-000C-6778	Sequence 6778, Ap	475	61.5	5.1	727	4	US-10-270-878-12	Sequence 12, Appli
403	62.5	5.2	233	3	US-09-485-737B-69	Sequence 69, Appli	476	61.5	5.1	775	1	US-07-966-278-1	Sequence 1, Appli
404	62.5	5.2	233	3	US-10-071-485-69	Sequence 69, Appli	477	61.5	5.1	775	1	US-08-424-921-1	Sequence 1, Appli
405	62.5	5.2	262	4	US-09-438-185A-30	Sequence 30, Appli	478	61.5	5.1	775	2	US-08-556-355A-1	Sequence 1, Appli
406	62.5	5.2	265	4	US-09-489-039A-12711	Sequence 12711, A	479	61.5	5.1	775	2	US-07-803-327A-1	Sequence 1, Appli
407	62.5	5.2	298	4	US-09-107-433-5121	Sequence 5121, Ap	480	61.5	5.1	775	4	US-09-244-889A-1	Sequence 1, Appli
408	62.5	5.2	328	4	US-09-583-110-4999	Sequence 4999, Ap	481	61.5	5.1	775	2	US-08-688-649-17	Sequence 37, Appli
409	62.5	5.2	344	3	US-09-120-365-63	Sequence 63, Appli	482	61.5	5.1	844	4	US-09-640-958-8	Sequence 8, Appli
410	62.5	5.2	344	3	US-09-515-039-63	Sequence 63, Appli	483	61.5	5.1	908	4	US-09-635-872A-15	Sequence 15, Appli
411	62.5	5.2	345	4	US-09-270-767-60654	Sequence 60654, A	484	61.5	5.1	908	4	US-09-636-077A-15	Sequence 15, Appli
412	62.5	5.2	404	4	US-09-270-767-45164	Sequence 45164, A	485	61.5	5.1	908	4	US-09-636-060C-15	Sequence 15, Appli
413	62.5	5.2	592	4	US-09-328-352-4438	Sequence 4438, Ap	486	61.5	5.1	908	4	US-09-986-552-15	Sequence 15, Appli
414	62.5	5.2	593	3	US-09-000-145-4	Sequence 4, Appli	487	61.5	5.1	908	4	US-09-636-596C-15	Sequence 15, Appli
415	62.5	5.2	603	4	US-09-252-991A-25038	Sequence 25038, A	488	61.5	5.1	908	4	US-10-023-894-9	Sequence 9, Appli
416	62.5	5.2	688	4	US-09-538-092-794	Sequence 794, App	489	61.5	5.1	908	4	US-10-306-686-15	Sequence 15, Appli
417	62.5	5.2	858	4	US-09-538-092-1127	Sequence 1127, Ap	490	61.5	5.1	927	3	US-08-895-601-6	Sequence 6, Appli
418	62.5	5.2	898	4	US-09-583-110-3750	Sequence 3750, Ap	491	61.5	5.1	946	4	US-09-902-540-16817	Sequence 16817, A
419	62.5	5.2	1008	4	US-09-949-016-10423	Sequence 10423, A	492	61.5	5.1	1809	3	US-09-012-515A-12	Sequence 12, Appli
420	62.5	5.2	1028	4	US-09-583-110-4290	Sequence 4290, Ap	493	61.5	5.1	1809	3	US-08-360-144A-12	Sequence 12, Appli
421	62.5	5.2	1030	4	US-09-107-433-2786	Sequence 2786, Ap	494	61.5	5.1	1809	4	US-09-012-504A-12	Sequence 12, Appli
422	62.5	5.2	1068	2	US-08-429-054A-11	Sequence 11, Appli	495	61.5	5.1	1809	4	US-09-012-399A-12	Sequence 12, Appli
423	62.5	5.2	1068	2	US-08-718-777-7	Sequence 7, Appli	496	61.5	5.1	1822	4	US-09-949-016-7999	Sequence 7999, Ap
424	62.5	5.2	1068	3	US-09-051-341-7	Sequence 7, Appli	497	61.5	5.1	2549	3	US-08-471-112A-3	Sequence 3, Appli
425	62.5	5.2	1068	4	US-09-394-272-8	Sequence 8, Appli	498	61.5	5.1	2549	4	US-09-950-634-3	Sequence 3, Appli
426	62.5	5.2	1068	4	US-08-429-053-11	Sequence 11, Appli	499	61.5	5.1	2549	4	US-09-538-092-1112	Sequence 1112, Ap
427	62.5	5.2	1275	4	US-09-949-016-11331	Sequence 11331, A	500	61.5	5.1	2549	5	PCT-US95-06722-12	Sequence 12, Appli
428	62.5	5.2	285	4	US-09-252-991A-17790	Sequence 17790, A	501	61	5.1	161	4	US-09-583-110-4752	Sequence 4752, Ap
429	62	5.1	72	3	US-09-060-726A-7	Sequence 7, Appli	502	61	5.1	166	4	US-09-107-433-3102	Sequence 3102, Ap
430	62	5.1	72	4	US-09-845-849A-7	Sequence 7, Appli	503	61	5.1	223	4	US-09-248-796A-23094	Sequence 23094, A
431	62	5.1	176	4	US-09-252-991A-30933	Sequence 30933, A	504	61	5.1	252	4	US-09-252-991A-30900	Sequence 30900, A
432	62	5.1	218	4	US-09-134-000C-4932	Sequence 4932, Ap	505	61	5.1	322	4	US-09-489-039A-8442	Sequence 8442, Ap
433	62	5.1	383	4	US-09-902-540-11160	Sequence 11160, A	506	61	5.1	332	4	US-09-489-039A-8365	Sequence 8365, Ap
434	62	5.1	410	4	US-09-949-016-7021	Sequence 7021, Ap	507	61	5.1	368	4	US-09-252-991A-19552	Sequence 19552, A
435	62	5.1	455	2	US-08-679-635A-5	Sequence 5, Appli	508	61	5.1	383	4	US-09-248-796A-20283	Sequence 20283, A
436	62	5.1	455	3	US-09-419-163-5	Sequence 5, Appli	509	61	5.1	386	4	US-09-328-352-8185	Sequence 8185, Ap
437	62	5.1	499	4	US-09-902-540-14146	Sequence 14146, A	510	61	5.1	397	5	PCT-US95-17111A-121	Sequence 121, App
438	62	5.1	554	4	US-09-198-452A-140	Sequence 140, App	511	61	5.1	495	4	US-09-252-991A-24607	Sequence 24607, A
439	62	5.1	621	4	US-09-489-039A-13909	Sequence 13909, A	512	61	5.1	496	4	US-09-339-1598-28	Sequence 28, Appli
440	62	5.1	663	4	US-09-252-991A-30843	Sequence 30843, A	513	61	5.1	497	4	US-09-181-339-3	Sequence 3, Appli
441	62	5.1	706	1	US-08-074-967-2	Sequence 2, Appli	514	61	5.1	560	2	US-08-808-931-18	Sequence 18, Appli
442	62	5.1	706	2	US-08-553-541B-2	Sequence 2, Appli	515	61	5.1	560	3	US-08-808-323-18	Sequence 18, Appli
443	62	5.1	706	3	US-09-268-202-2	Sequence 2, Appli	516	61	5.1	560	3	US-09-050-603A-18	Sequence 18, Appli
444	62	5.1	706	4	US-09-761-117-2	Sequence 2, Appli	517	61	5.1	560	3	US-09-102-4208-18	Sequence 18, Appli
445	62	5.1	706	5	PCT-US94-06669-2	Sequence 2, Appli	518	61	5.1	560	3	US-09-497-698-18	Sequence 18, Appli
446	62	5.1	755	3	US-09-097-767A-38	Sequence 38, Appli	519	61	5.1	560	4	US-09-730-525-18	Sequence 18, Appli
447	62	5.1	826	4	US-09-134-000C-4999	Sequence 4999, Ap	520	61	5.1	565	4	US-09-252-991A-28571	Sequence 28571, A
448	62	5.1	829	4	US-09-902-540-11104	Sequence 11104, Ap	521	61	5.1	639	4	US-09-949-016-6812	Sequence 6812, Ap
449	62	5.1	830	4	US-09-252-991A-32609	Sequence 32609, A	522	61	5.1	652	4	US-09-949-016-7323	Sequence 7323, A
450	62	5.1	1130	4	US-09-538-092-894	Sequence 834, App	523	61	5.1	660	4	US-09-252-991A-22842	Sequence 22842, A
451	62	5.1	1148	4	US-09-949-016-6798	Sequence 6798, Ap	524	61	5.1	710	1	US-08-162-809-22	Sequence 22, Appli
452	62	5.1	1169	4	US-09-949-016-9630	Sequence 9630, Ap	525	61	5.1	722	1	US-08-162-809-4	Sequence 4, Appli
453	62	5.1	1286	4	US-09-252-991A-44589	Sequence 24589, A	526	61	5.1	744	1	US-08-162-809-20	Sequence 20, Appli
454	62	5.1	1507	3	US-08-929-329-5	Sequence 5, Appli	527	61	5.1	774	3	US-08-902-632-2	Sequence 2, Appli
455	61.5	5.1	235	4	US-09-011-769A-27	Sequence 27, Appli	528	61	5.1	774	3	US-09-073-354-1	Sequence 1, Appli
456	61.5	5.1	271	1	US-09-328-352-6285	Sequence 6285, Ap	529	61	5.1	774	3	US-08-656-005A-1	Sequence 1, Appli
457	61.5	5.1	271	1	US-07-914-282D-4	Sequence 4, Appli	530	61	5.1	774	3	US-09-073-259-1	Sequence 1, Appli
458	61.5	5.1	271	1	US-08-276-887A-4	Sequence 4, Appli	531	61	5.1	774	3	US-09-363-095-1	Sequence 1, Appli
459	61.5	5.1	271	1	PCT-US93-02460-4	Sequence 4, Appli	532	61	5.1	774	3	US-09-418-027-1	Sequence 1, Appli
460	61.5	5.1	285	4	US-09-252-991A-29780	Sequence 29780, A	533	61	5.1	779	1	US-08-375-134-12	Sequence 12, Appli
461	61.5	5.1	291	4	US-09-902-540-10710	Sequence 10710, A	534	61	5.1	779	5	PCT-US95-15263-12	Sequence 12, Appli
462	61.5	5.1	292	4	US-09-489-039A-12760	Sequence 12760, A	535	61	5.1	2317	4	US-09-949-016-10109	Sequence 10109, A
463	61.5	5.1	297	4	US-09-543-681A-8242	Sequence 8242, Ap	536	61	5.1	2680	4	US-09-489-039A-7973	Sequence 7973, Ap
464	61.5	5.1	349	4	US-09-248-796A-16744	Sequence 16744, A	537	61	5.1	2680	4	US-08-826-267-2	Sequence 2, Appli
465	61.5	5.1	388	4	US-09-252-991A-21572	Sequence 21572, A	538	60.5	5.0	193	4	US-09-949-016-7888	Sequence 7888, Ap

539	60.5	5.0	197	4	US-09-252-991A-27889	Sequence 27889, A	612	60	5.0	608	3	US-09-134-001C-3395	Sequence 3395, Ap
540	60.5	5.0	202	4	US-09-902-540-11464	Sequence 11464, A	613	60	5.0	634	1	US-07-688-352C-22	Sequence 22, Appl
541	60.5	5.0	205	4	US-09-907-794A-23	Sequence 23, Appl	614	60	5.0	658	4	US-09-902-540-14501	Sequence 14501, A
542	60.5	5.0	205	4	US-09-905-125A-23	Sequence 23, Appl	615	60	5.0	673	3	US-09-091-725-23	Sequence 23, Appl
543	60.5	5.0	205	4	US-09-902-775A-23	Sequence 23, Appl	616	60	5.0	666	2	US-08-942-521B-9	Sequence 9, Appl
544	60.5	5.0	205	4	US-09-906-700-23	Sequence 23, Appl	617	60	5.0	734	3	US-09-146-249A-85	Sequence 85, Appl
545	60.5	5.0	205	4	US-09-903-603A-23	Sequence 23, Appl	618	60	5.0	724	3	US-08-206-188B-85	Sequence 85, Appl
546	60.5	5.0	205	4	US-09-904-920A-23	Sequence 23, Appl	619	60	5.0	886	2	US-08-474-379C-65	Sequence 65, Appl
547	60.5	5.0	205	4	US-09-909-064-23	Sequence 23, Appl	620	60	5.0	886	3	US-09-146-249A-65	Sequence 65, Appl
548	60.5	5.0	205	4	US-09-905-381A-23	Sequence 23, Appl	621	60	5.0	886	3	US-08-306-188B-65	Sequence 65, Appl
549	60.5	5.0	205	4	US-09-906-618-23	Sequence 23, Appl	622	60	5.0	888	2	US-08-474-379C-12	Sequence 12, Appl
550	60.5	5.0	212	3	US-09-036-985A-2	Sequence 2, Appl	623	60	5.0	888	3	US-09-146-249A-12	Sequence 12, Appl
551	60.5	5.0	224	4	US-09-456-090A-40	Sequence 40, Appl	624	60	5.0	888	3	US-08-206-188B-12	Sequence 12, Appl
552	60.5	5.0	224	4	US-09-453-234-40	Sequence 40, Appl	625	60	5.0	900	1	US-07-688-352C-12	Sequence 12, Appl
553	60.5	5.0	235	4	US-09-893-737-92	Sequence 232, Ap	626	60	5.0	901	4	US-09-917-254-93	Sequence 93, Appl
554	60.5	5.0	239	3	US-08-812-586-39	Sequence 23, Appl	627	60	5.0	1037	4	US-09-252-991A-16796	Sequence 16796, A
555	60.5	5.0	239	4	US-09-535-832A-30	Sequence 30, Appl	628	60	5.0	1438	4	US-09-538-092-189	Sequence 189, Ap
556	60.5	5.0	258	4	US-09-328-352-8149	Sequence 8149, Ap	629	60	5.0	1903	4	US-09-949-016-8049	Sequence 8049, Ap
557	60.5	5.0	370	2	US-08-341-538A-2	Sequence 2, Appl	630	60	5.0	1912	3	US-08-913-832A-2	Sequence 2, Appl
558	60.5	5.0	370	2	US-08-725-518-2	Sequence 2, Appl	631	60	5.0	1912	3	US-09-249-181A-2	Sequence 2, Appl
559	60.5	5.0	370	4	US-09-538-092-1286	Sequence 1286, Ap	632	60	5.0	1912	4	US-09-158-707-2	Sequence 2, Appl
560	60.5	5.0	370	4	US-09-949-016-6581	Sequence 6581, Ap	633	60	5.0	1987	4	US-09-949-016-6275	Sequence 6275, Ap
561	60.5	5.0	376	4	US-09-949-016-11385	Sequence 11385, A	634	60	5.0	2183	3	US-08-746-111-5	Sequence 5, Appl
562	60.5	5.0	380	3	US-08-468-846-2	Sequence 2, Appl	635	60	5.0	2375	4	US-09-538-092-1131	Sequence 1131, Ap
563	60.5	5.0	380	3	US-08-915-096A-2	Sequence 2, Appl	636	60	5.0	2375	4	US-09-621-976-6877	Sequence 6877, Ap
564	60.5	5.0	381	4	US-09-248-796A-16356	Sequence 16356, A	637	60	5.0	112	3	US-09-060-726A-5	Sequence 5, Appl
565	60.5	5.0	384	4	US-09-949-016-9661	Sequence 9661, Ap	638	60	5.0	182	2	US-08-698-805-4	Sequence 4, Appl
566	60.5	5.0	386	4	US-09-248-796A-17565	Sequence 17565, A	639	59.5	4.9	210	4	US-09-902-540-12645	Sequence 12645, A
567	60.5	5.0	425	4	US-09-500-495A-6	Sequence 6, Appl	640	59.5	4.9	219	4	US-09-902-540-12645	Sequence 12672, A
568	60.5	5.0	427	4	US-09-248-796A-17709	Sequence 17709, A	641	59.5	4.9	228	4	US-09-270-767-34872	Sequence 34872, A
569	60.5	5.0	453	4	US-09-543-681A-6645	Sequence 6645, Ap	642	59.5	4.9	228	4	US-09-270-767-34872	Sequence 34872, A
570	60.5	5.0	472	3	US-08-985-492-13	Sequence 13, Appl	643	59.5	4.9	234	4	US-09-740-002-24	Sequence 24, Appl
571	60.5	5.0	541	4	US-09-252-991A-32947	Sequence 32947, A	644	59.5	4.9	221	4	US-09-461-325-199	Sequence 199, Ap
572	60.5	5.0	579	4	US-09-252-991A-18063	Sequence 18063, A	645	59.5	4.9	221	4	US-10-012-542-199	Sequence 199, Ap
573	60.5	5.0	643	4	US-09-252-991A-17181	Sequence 17181, A	646	59.5	4.9	271	4	US-10-115-123-199	Sequence 199, Ap
574	60.5	5.0	667	3	US-08-959-004-11	Sequence 11, Appl	647	59.5	4.9	306	3	US-09-392-772-6	Sequence 6, Appl
575	60.5	5.0	668	4	US-09-252-991A-19879	Sequence 19879, A	648	59.5	4.9	332	3	US-09-134-001C-3194	Sequence 3194, Ap
576	60.5	5.0	824	4	US-09-134-000C-4908	Sequence 4908, Ap	649	59.5	4.9	337	4	US-09-949-016-9200	Sequence 9200, Ap
577	60.5	5.0	864	4	US-09-751-687-18	Sequence 18, Appl	650	59.5	4.9	337	4	US-09-949-016-9201	Sequence 9201, Ap
578	60.5	5.0	1088	4	US-09-252-991A-27278	Sequence 27278, A	651	59.5	4.9	337	4	US-09-949-016-9202	Sequence 9202, Ap
579	60.5	5.0	1226	1	US-08-280-443-2	Sequence 2, Appl	652	59.5	4.9	337	4	US-09-949-016-9203	Sequence 9203, Ap
580	60.5	5.0	1226	1	US-08-457-459-2	Sequence 2, Appl	653	59.5	4.9	337	4	US-09-949-016-9204	Sequence 9204, Ap
581	60.5	5.0	1226	1	US-08-555-678-2	Sequence 2, Appl	654	59.5	4.9	337	4	US-09-949-016-9205	Sequence 9205, Ap
582	60.5	5.0	1226	5	PCT-US95-02375-2	Sequence 2, Appl	655	59.5	4.9	337	4	US-09-949-016-9206	Sequence 9206, Ap
583	60.5	5.0	1953	4	US-09-917-254-92	Sequence 92, Appl	656	59.5	4.9	337	3	US-08-857-076-100	Sequence 100, Ap
584	60.5	5.0	2396	1	US-08-157-005-2	Sequence 2, Appl	657	59.5	4.9	372	4	US-09-252-991A-29108	Sequence 29108, A
585	60.5	5.0	2396	3	US-08-747-863-2	Sequence 2, Appl	658	59.5	4.9	337	4	US-09-252-991A-20113	Sequence 20113, A
586	60.5	5.0	2396	4	US-09-565-864-2	Sequence 2, Appl	659	59.5	4.9	419	4	US-09-252-991A-31409	Sequence 31409, A
587	60.5	5.0	2396	4	US-10-226-065-2	Sequence 2, Appl	660	59.5	4.9	459	4	US-09-252-991A-26783	Sequence 26783, A
588	60.5	5.0	2549	4	US-08-265-967C-1	Sequence 1, Appl	661	59.5	4.9	476	3	US-08-624-635-5	Sequence 5, Appl
589	60.5	5.0	2549	4	US-08-305-790B-2	Sequence 2, Appl	662	59.5	4.9	485	4	US-09-949-016-10440	Sequence 10440, A
590	60	5.0	119	4	US-09-902-540-12746	Sequence 12746, A	663	59.5	4.9	483	4	US-09-328-352-6663	Sequence 6663, Ap
591	60	5.0	186	4	US-09-543-681A-4427	Sequence 4427, Ap	664	59.5	4.9	553	4	US-09-949-016-10362	Sequence 10362, A
592	60	5.0	186	4	US-09-540-236-3237	Sequence 3237, Ap	665	59.5	4.9	609	4	US-09-949-016-7747	Sequence 7747, Ap
593	60	5.0	198	4	US-09-248-796A-16423	Sequence 16423, A	666	59.5	4.9	609	4	US-09-949-016-7748	Sequence 7748, Ap
594	60	5.0	262	4	US-09-902-540-15602	Sequence 15602, A	667	59.5	4.9	609	4	US-09-949-016-7749	Sequence 7749, Ap
595	60	5.0	302	5	PCT-US91-02714-21	Sequence 21, Appl	668	59.5	4.9	609	4	US-09-949-016-7750	Sequence 7750, Ap
596	60	5.0	352	4	US-09-134-000C-5243	Sequence 5243, Ap	669	59.5	4.9	609	4	US-09-949-016-7751	Sequence 7751, Ap
597	60	5.0	398	2	US-08-474-379C-86	Sequence 86, Appl	670	59.5	4.9	609	4	US-09-949-016-7752	Sequence 7752, Ap
598	60	5.0	414	4	US-09-107-532A-6114	Sequence 6114, Ap	671	59.5	4.9	609	4	US-09-949-016-7753	Sequence 7753, Ap
599	60	5.0	422	3	US-09-217-228-7	Sequence 7, Appl	672	59.5	4.9	609	4	US-09-949-016-7754	Sequence 7754, Ap
600	60	5.0	424	4	US-08-311-731A-220	Sequence 220, App	673	59.5	4.9	619	4	US-09-538-092-94	Sequence 94, Appl
601	60	5.0	445	4	US-09-949-016-11396	Sequence 11396, A	674	59.5	4.9	653	4	US-09-252-991A-16802	Sequence 16802, A
602	60	5.0	478	4	US-09-270-767-43204	Sequence 43204, A	675	59.5	4.9	662	3	US-09-061-768A-25	Sequence 25, Appl
603	60	5.0	513	4	US-09-252-991A-17606	Sequence 17606, A	676	59.5	4.9	662	4	US-09-764-246-25	Sequence 25, Appl
604	60	5.0	518	4	US-09-595-857B-30	Sequence 30, Appl	677	59.5	4.9	697	4	US-09-252-991A-32689	Sequence 32689, A
605	60	5.0	535	4	US-09-949-016-6847	Sequence 6847, Ap	678	59.5	4.9	804	3	US-08-981-446B-3	Sequence 3, Appl
606	60	5.0	542	3	US-08-675-816-6	Sequence 6, Appl	679	59.5	4.9	1034	4	US-09-252-991A-20969	Sequence 20969, A
607	60	5.0	552	4	US-09-773-426A-9	Sequence 9, Appl	680	59.5	4.9	1058	4	US-09-583-110-4522	Sequence 4522, Ap
608	60	5.0	552	4	US-10-314-881-9	Sequence 9, Appl	681	59.5	4.9	1058	4	US-09-433-4164	Sequence 4164, Ap
609	60	5.0	552	4	US-09-902-540-15502	Sequence 15502, A	682	59.5	4.9	1066	4	US-10-160-719A-18	Sequence 18, Appl
610	60	5.0	599	4	US-09-252-991A-17250	Sequence 17250, A	683	59.5	4.9	1066	4	US-10-160-719A-38	Sequence 38, Appl
611	60	5.0	605	4	US-09-949-016-9305	Sequence 9305, Ap	684	59.5	4.9	1164	4	US-09-949-016-9269	Sequence 9269, Ap

685	59.5	4.9	1261	4	US-09-248-796A-16620	Sequence 16620, A	758	58.5	4.9	182	4	US-09-489-039A-8631	Sequence 8631, Ap
686	59.5	4.9	1463	4	US-09-445-353B-3	Sequence 3, Appl1	759	58.5	4.9	190	4	US-09-252-991A-20376	Sequence 20376, A
687	59.5	4.9	1992	4	US-09-538-092-1327	Sequence 1327, Ap	760	58.5	4.9	218	4	US-09-698-705-12	Sequence 12, Appl
688	59	4.9	59	4	US-09-270-767-60687	Sequence 60687, A	761	58.5	4.9	236	1	US-08-157-101A-5	Sequence 5, Appl1
689	4.9	4.9	111	4	US-09-149-476-673	Sequence 673, App	762	58.5	4.9	250	4	US-09-540-236-052	Sequence 2052, Ap
690	59	4.9	145	4	US-09-489-039A-8799	Sequence 8799, Ap	763	58.5	4.9	260	4	US-09-252-991A-29015	Sequence 29015, A
691	59	4.9	142	4	US-09-252-991A-8260	Sequence 22630, A	764	58.5	4.9	261	4	US-09-252-991A-24007	Sequence 24007, A
692	59	4.9	155	3	US-09-134-001C-3243	Sequence 3243, Ap	765	58.5	4.9	265	3	US-09-310-463-34	Sequence 34, Appl
693	59	4.9	170	3	US-09-228-986-116	Sequence 116, App	766	58.5	4.9	280	4	US-09-902-540-11498	Sequence 11498, A
694	59	4.9	170	3	US-10-101-464A-116	Sequence 116, App	767	58.5	4.9	281	4	US-09-543-681A-4460	Sequence 4460, Ap
695	4.9	4.9	227	4	US-09-489-039A-10192	Sequence 10192, A	768	58.5	4.9	282	1	US-07-712-476A-5	Sequence 5, Appl1
696	4.9	4.9	227	4	US-09-994-427A-7	Sequence 7, Appli	769	58.5	4.9	292	4	US-09-583-110-3511	Sequence 3511, Ap
697	59	4.9	239	4	US-10-000-469-8	Sequence 8, Appli	770	58.5	4.9	296	1	US-07-712-476A-1	Sequence 1, Appl1
698	59	4.9	253	4	US-09-489-039A-13477	Sequence 13477, A	771	58.5	4.9	299	3	US-09-310-463-30	Sequence 30, Appl
699	59	4.9	256	4	US-09-248-796A-15990	Sequence 15990, A	772	58.5	4.9	300	4	US-09-107-433-1340	Sequence 4340, Ap
700	59	4.9	268	3	US-08-836-134-22	Sequence 22, Appl	773	58.5	4.9	300	6	Sequence 5962, Ap	
701	59	4.9	268	3	US-09-493-784-22	Sequence 22, Appl	774	58.5	4.9	300	6	Patent No. 5340934	
702	59	4.9	277	1	US-08-762-129-5	Sequence 5, Appli	775	58.5	4.9	300	6	Patent No. 5340934	
703	59	4.9	277	4	US-09-948-016-6126	Sequence 6126, Ap	776	58.5	4.9	311	6	Patent No. 5340934	
704	59	4.9	293	4	US-09-902-540-16212	Sequence 16212, A	777	58.5	4.9	312	3	US-09-710-379-2450	Sequence 2450, Ap
705	59	4.9	295	3	US-09-037-143-50	Sequence 50, Appl	778	58.5	4.9	314	4	US-09-821-736-5	Sequence 5, Appl
706	59	4.9	295	3	US-08-260-174-50	Sequence 50, Appl	779	58.5	4.9	314	4	US-09-134-253-1	Sequence 1, Appl1
707	59	4.9	295	3	US-09-338-128A-50	Sequence 50, Appl	780	58.5	4.9	314	4	US-09-206-576-2	Sequence 2, Appl1
708	59	4.9	295	3	US-09-232-346-50	Sequence 50, Appl	781	58.5	4.9	318	3	US-09-538-092-896	Sequence 896, App
709	59	4.9	308	4	US-09-948-016-11042	Sequence 11042, A	782	58.5	4.9	318	3	US-09-134-001C-3380	Sequence 3380, Ap
710	59	4.9	324	4	US-09-107-532A-6145	Sequence 6145, Ap	783	58.5	4.9	324	4	US-09-902-540-14236	Sequence 14236, A
711	59	4.9	325	4	US-09-134-000C-4346	Sequence 4346, Ap	784	58.5	4.9	333	1	US-09-949-016-10363	Sequence 10363, A
712	59	4.9	334	4	US-09-328-859-2	Sequence 2, Appli	785	58.5	4.9	333	1	US-07-991-587A-2	Sequence 2, Appl1
713	59	4.9	336	4	US-09-252-991A-17393	Sequence 17393, A	786	58.5	4.9	344	4	US-08-309-985-2	Sequence 2, Appl1
714	59	4.9	440	4	US-09-949-016-10042	Sequence 10042, A	787	58.5	4.9	354	4	US-09-270-767-13505	Sequence 43505, A
715	59	4.9	448	4	US-09-543-681A-7737	Sequence 7737, Ap	788	58.5	4.9	378	3	US-09-608-917A-2	Sequence 2, Appl
716	59	4.9	460	4	US-09-826-509-513	Sequence 513, App	789	58.5	4.9	378	4	US-09-500-569-10	Sequence 10, Appl
717	59	4.9	469	4	US-09-252-991A-25438	Sequence 25438, A	790	58.5	4.9	386	4	US-09-971-823B-10	Sequence 10, Appl
718	59	4.9	474	3	US-09-312-041-5	Sequence 5, Appl1	791	58.5	4.9	400	2	US-09-489-039A-8771	Sequence 8771, Ap
719	59	4.9	479	1	US-08-767-993-7	Sequence 7, Appli	792	58.5	4.9	409	4	US-08-624-601-8	Sequence 8, Appl1
720	59	4.9	479	1	US-08-313-553-7	Sequence 7, Appli	793	58.5	4.9	411	4	US-09-880-137-7	Sequence 7, Appl1
721	59	4.9	506	4	US-09-489-039A-8921	Sequence 8921, Ap	794	58.5	4.9	413	4	US-09-402-532-2	Sequence 2, Appl1
722	59	4.9	516	3	US-09-197-063-2	Sequence 22, Appl	795	58.5	4.9	413	4	US-09-949-016-7602	Sequence 7602, Ap
723	59	4.9	530	4	US-09-252-991A-20846	Sequence 20846, A	796	58.5	4.9	414	4	US-09-402-532-5	Sequence 7603, Ap
724	59	4.9	540	4	US-09-252-991A-30388	Sequence 30388, A	797	58.5	4.9	421	3	US-09-020-846-68	Sequence 5, Appl1
725	59	4.9	541	4	US-08-828-159A-2	Sequence 2, Appli	798	58.5	4.9	429	4	US-09-252-991A-29792	Sequence 29792, A
726	59	4.9	552	1	US-07-999-280A-22	Sequence 22, Appl	799	58.5	4.9	444	4	US-09-402-532-7	Sequence 7, Appli
727	59	4.9	552	1	US-08-426-279-22	Sequence 22, Appl	800	58.5	4.9	454	4	US-09-902-540-15865	Sequence 15865, A
728	59	4.9	552	1	US-08-401-013-22	Sequence 22, Appl	801	58.5	4.9	467	4	US-09-252-991A-27314	Sequence 27314, A
729	59	4.9	552	3	US-08-426-570-22	Sequence 22, Appl	802	58.5	4.9	471	1	US-08-203-905B-2	Sequence 2, Appl1
730	59	4.9	552	3	US-08-426-876-22	Sequence 22, Appl	803	58.5	4.9	471	1	US-09-949-016-6774	Sequence 6774, Ap
731	59	4.9	552	3	US-08-426-243-22	Sequence 22, Appl	804	58.5	4.9	472	1	US-08-749-903-3	Sequence 3, Appl1
732	59	4.9	552	3	US-08-401-632-22	Sequence 22, Appl	805	58.5	4.9	472	1	US-09-088-641-3	Sequence 3, Appl1
733	59	4.9	573	4	US-09-328-352-6016	Sequence 6016, Ap	806	58.5	4.9	477	3	US-08-704-711A-20	Sequence 20, Appl
734	59	4.9	573	4	US-09-489-039A-12091	Sequence 12091, A	807	58.5	4.9	477	3	US-08-448-189-15	Sequence 15, Appl
735	59	4.9	612	4	US-09-902-540-9694	Sequence 9694, Ap	808	58.5	4.9	477	3	US-08-281-513-1	Sequence 9, Appl
736	59	4.9	614	4	US-09-252-991A-19833	Sequence 19833, A	809	58.5	4.9	477	3	US-09-521-220-20	Sequence 20, Appl
737	59	4.9	636	4	US-09-949-016-11656	Sequence 11656, A	810	58.5	4.9	477	3	US-09-391-104-21	Sequence 21, Appl
738	59	4.9	728	4	US-09-949-016-8296	Sequence 8296, Ap	811	58.5	4.9	477	4	US-09-689-730-15	Sequence 15, Appl
739	59	4.9	769	1	US-08-243-542-4	Sequence 4, Appli	812	58.5	4.9	481	4	US-09-543-681A-4726	Sequence 4726, Ap
740	59	4.9	769	1	US-08-477-407-4	Sequence 4, Appli	813	58.5	4.9	483	4	US-09-949-016-11046	Sequence 11046, A
741	59	4.9	769	1	US-08-484-355-4	Sequence 4, Appli	814	58.5	4.9	503	4	US-09-657-013-50	Sequence 50, Appl
742	59	4.9	769	1	US-09-949-016-9605	Sequence 9605, Ap	815	58.5	4.9	512	3	US-09-350-234-24	Sequence 24, Appl
743	59	4.9	769	4	US-09-949-016-9606	Sequence 9606, Ap	816	58.5	4.9	512	4	US-09-603-311-24	Sequence 24, Appl
744	59	4.9	828	4	US-09-107-532A-4191	Sequence 4191, Ap	817	58.5	4.9	512	4	US-09-570-856B-30	Sequence 30, Appl
745	59	4.9	917	4	US-09-902-540-12845	Sequence 12845, A	818	58.5	4.9	549	4	US-09-657-013-54	Sequence 54, Appl
746	59	4.9	929	4	US-09-697-022-3	Sequence 3, Appli	819	58.5	4.9	549	4	US-09-949-016-8881	Sequence 8881, Ap
747	59	4.9	966	2	US-08-868-786-2	Sequence 2, Appli	820	58.5	4.9	549	4	US-09-949-016-8882	Sequence 8882, Ap
748	59	4.9	981	2	US-08-649-046-2	Sequence 2, Appli	821	58.5	4.9	549	4	US-09-949-016-8883	Sequence 8883, Ap
749	59	4.9	1044	4	US-10-101-464A-956	Sequence 956, App	822	58.5	4.9	549	4	US-09-949-016-8884	Sequence 8884, Ap
750	59	4.9	1217	4	US-09-949-016-7454	Sequence 7454, Ap	823	58.5	4.9	549	4	US-09-949-016-8885	Sequence 8885, Ap
751	59	4.9	4150	3	US-09-428-517-2	Sequence 2, Appli	824	58.5	4.9	551	4	US-09-252-991A-20358	Sequence 20358, A
752	58.5	4.9	92	4	US-09-270-767-34271	Sequence 34271, A	825	58.5	4.9	574	3	US-09-079-431B-6	Sequence 6, Appli
753	58.5	4.9	92	4	US-09-270-767-49488	Sequence 49488, A	826	58.5	4.9	595	4	US-09-949-016-8871	Sequence 8871, Ap
754	58.5	4.9	124	4	US-09-902-540-16378	Sequence 16378, A	827	58.5	4.9	595	4	US-09-949-016-8872	Sequence 8872, Ap
755	58.5	4.9	138	4	US-09-252-991A-17424	Sequence 17424, A	828	58.5	4.9	595	4	US-09-949-016-8873	Sequence 8873, Ap
756	58.5	4.9	169	4	US-09-134-000C-5588	Sequence 5588, Ap	829	58.5	4.9	595	4	US-09-949-016-8874	Sequence 8874, Ap
757	58.5	4.9	180	4	US-09-949-016-6478	Sequence 6478, Ap	830	58.5	4.9	595	4	US-09-949-016-8875	Sequence 8875, Ap

831	58.5	4.9	638	3	US-09-347-488-2	Sequence 2, Appli	904	58	4.8	541	4	US-09-583-110-2955	Sequence 2859, Ap
832	58.5	4.9	639	3	US-09-376-856-2	Sequence 2, Appli	905	58	4.8	552	1	US-07-999-280A-24	Sequence 24, Appl
833	58.5	4.9	639	3	US-09-107-532A-5989	Sequence 5989, Ap	906	58	4.8	552	1	US-08-426-279-24	Sequence 24, Appl
834	58.5	4.9	721	3	US-09-390-234-50	Sequence 20, Appl	907	58	4.8	552	1	US-08-401-013-24	Sequence 24, Appl
835	58.5	4.9	721	4	US-09-603-311-50	Sequence 20, Appl	908	58	4.8	552	3	US-08-426-570-24	Sequence 24, Appl
836	58.5	4.9	731	4	US-09-252-991A-17180	Sequence 17180, A	909	58	4.8	552	3	US-08-425-876-24	Sequence 24, Appl
837	58.5	4.9	746	3	US-09-149-934-4	Sequence 4, Appli	910	58	4.8	552	3	US-08-426-243-24	Sequence 24, Appl
838	58.5	4.9	804	3	US-08-855-910-4	Sequence 4, Appli	911	58	4.8	552	3	US-08-401-632-24	Sequence 24, Appl
839	58.5	4.9	848	4	US-09-538-092-53	Sequence 33, Appl	912	58	4.8	556	4	US-09-107-433-3006	Sequence 3006, Ap
840	58.5	4.9	997	4	US-09-198-452A-602	Sequence 602, App	913	58	4.8	553	4	US-09-540-236-2898	Sequence 2898, Ap
841	58.5	4.9	1006	4	US-09-949-016-8421	Sequence 8421, Ap	914	58	4.8	555	4	US-09-252-991A-25815	Sequence 25815, A
842	58.5	4.9	1006	4	US-09-949-016-8530	Sequence 8530, Ap	915	58	4.8	630	4	US-10-003-392-16	Sequence 16, Appl
843	58.5	4.9	1014	4	US-10-101-464A-807	Sequence 807, Ap	916	58	4.8	632	4	US-09-540-236-2216	Sequence 2216, Ap
844	58.5	4.9	1405	4	US-09-438-185A-566	Sequence 566, App	917	58	4.8	679	4	US-09-050-516-42	Sequence 42, Appl
845	58.5	4.9	1454	4	US-09-949-016-7599	Sequence 7599, Ap	918	58	4.8	679	4	US-10-278-547-42	Sequence 42, Appl
846	58.5	4.9	1454	4	US-09-949-016-7600	Sequence 7600, Ap	919	58	4.8	729	4	US-09-328-352-7603	Sequence 7603, Ap
847	58.5	4.9	2216	4	US-09-902-540-12221	Sequence 12221, A	920	58	4.8	735	2	US-08-765-243-6	Sequence 6, Appli
848	58.5	4.9	2584	3	US-08-936-135-4	Sequence 4, Appli	921	58	4.8	735	5	PCT-US95-07295-6	Sequence 6, Appli
849	58	4.8	79	1	US-08-221-285-33	Sequence 33, Appl	922	58	4.8	736	4	US-09-949-016-6807	Sequence 6807, Ap
850	58	4.8	79	3	US-08-428-596A-33	Sequence 33, Appl	923	58	4.8	736	4	US-10-144-198-38	Sequence 38, Appl
851	58	4.8	81	2	US-08-812-003-2	Sequence 2, Appli	924	58	4.8	769	4	US-09-489-039A-12201	Sequence 12201, A
852	58	4.8	154	4	US-09-543-681A-5343	Sequence 5343, Ap	925	58	4.8	773	4	US-09-270-767-33141	Sequence 33141, A
853	58	4.8	158	4	US-09-252-991A-24852	Sequence 24852, A	926	58	4.8	773	4	US-09-270-767-48358	Sequence 48358, A
854	58	4.8	162	4	US-09-252-991A-25771	Sequence 25771, A	927	58	4.8	786	4	US-10-144-198-18	Sequence 18, Appl
855	58	4.8	182	4	US-09-107-532A-5701	Sequence 5701, Ap	928	58	4.8	786	4	US-10-029-180-52	Sequence 52, Appl
856	58	4.8	190	4	US-09-583-110-3050	Sequence 3050, Ap	929	58	4.8	808	4	US-09-270-767-36557	Sequence 36557, A
857	58	4.8	191	4	US-09-538-092-118	Sequence 118, App	930	58	4.8	808	4	US-09-270-767-51774	Sequence 51774, A
858	58	4.8	204	4	US-09-107-433-4425	Sequence 4425, Ap	931	58	4.8	840	4	US-10-030-330-5	Sequence 5, Appli
859	58	4.8	221	4	US-09-902-540-12858	Sequence 12858, A	932	58	4.8	879	3	US-08-794-158-2	Sequence 2, Appli
860	58	4.8	226	4	US-09-328-352-1169	Sequence 7169, Ap	933	58	4.8	912	4	US-09-902-540-16181	Sequence 16181, A
861	58	4.8	234	3	US-09-049-672A-2	Sequence 2, Appli	934	58	4.8	964	4	US-09-328-352-6926	Sequence 6926, Ap
862	58	4.8	241	4	US-09-270-767-42375	Sequence 42375, A	935	58	4.8	966	4	US-09-657-931A-12	Sequence 12, Appl
863	58	4.8	246	4	US-09-558-284-2	Sequence 2, Appli	936	58	4.8	1051	4	US-09-949-016-6190	Sequence 6190, Ap
864	58	4.8	251	4	US-09-640-211A-1019	Sequence 1019, Ap	937	58	4.8	1054	4	US-09-626-301-2	Sequence 2, Appli
865	58	4.8	251	4	US-09-489-039A-9020	Sequence 9020, Ap	938	58	4.8	1059	4	US-09-252-991A-28189	Sequence 28189, A
866	58	4.8	263	4	US-09-270-767-57554	Sequence 57554, A	939	58	4.8	1066	4	US-09-949-016-6617	Sequence 6617, Ap
867	58	4.8	263	4	US-09-543-681A-5138	Sequence 5138, Ap	940	58	4.8	1088	4	US-09-949-016-6644	Sequence 6644, Ap
868	58	4.8	275	4	US-09-328-352-7552	Sequence 7552, Ap	941	58	4.8	1090	4	US-09-949-016-9725	Sequence 9725, Ap
869	58	4.8	332	4	US-09-248-796A-15797	Sequence 15797, A	942	58	4.8	1090	4	US-09-949-016-9726	Sequence 9726, Ap
870	58	4.8	332	4	US-09-902-540-12515	Sequence 12515, A	943	58	4.8	1119	4	US-09-543-681A-8019	Sequence 8019, Ap
871	58	4.8	337	2	US-08-861-464-12	Sequence 12, Appl	944	58	4.8	1119	4	US-09-949-016-9459	Sequence 9459, Ap
872	58	4.8	337	2	US-08-396-001-12	Sequence 12, Appl	945	58	4.8	1147	4	US-09-949-016-8616	Sequence 8616, Ap
873	58	4.8	337	3	US-09-323-433A-12	Sequence 12, Appl	946	58	4.8	1971	4	US-09-914-272A-1	Sequence 1, Appli
874	58	4.8	337	3	US-09-826-752-12	Sequence 12, Appl	947	58	4.8	1971	4	US-10-638-333-1	Sequence 1, Appli
875	58	4.8	349	3	US-09-343-011B-1	Sequence 1, Appli	948	58	4.8	246	3	US-09-125-028-2	Sequence 2, Appli
876	58	4.8	351	1	US-08-324-483-2	Sequence 2, Appli	949	58	4.8	246	3	US-08-894-444C-2	Sequence 2, Appli
877	58	4.8	361	4	US-09-270-767-37733	Sequence 37733, A	950	58	4.8	2958	4	US-09-919-497-70	Sequence 70, Appl
878	58	4.8	365	4	US-09-134-000C-4369	Sequence 4369, Ap	951	58	4.8	5087	3	US-09-144-085-1	Sequence 1, Appli
879	58	4.8	380	4	US-09-248-796A-17008	Sequence 17008, A	952	57.5	4.8	62	4	US-09-248-796A-24014	Sequence 24014, A
880	58	4.8	384	4	US-09-489-039A-13733	Sequence 13733, A	953	57.5	4.8	132	2	US-08-616-392C-10	Sequence 10, Appl
881	58	4.8	394	4	US-09-252-991A-19674	Sequence 19674, A	954	57.5	4.8	224	4	US-09-456-090A-52	Sequence 52, Appl
882	58	4.8	402	4	US-09-270-767-42272	Sequence 42272, A	955	57.5	4.8	224	4	US-09-453-234-52	Sequence 52, Appl
883	58	4.8	433	4	US-09-673-899-2	Sequence 2, Appli	956	57.5	4.8	226	4	US-09-456-090A-42	Sequence 42, Appl
884	58	4.8	433	4	US-09-673-899-4	Sequence 4, Appli	957	57.5	4.8	226	4	US-09-456-090A-80	Sequence 80, Appl
885	58	4.8	433	4	US-09-673-899-6	Sequence 6, Appli	958	57.5	4.8	226	4	US-09-453-234-40	Sequence 42, Appl
886	58	4.8	438	4	US-09-252-991A-19012	Sequence 19012, A	959	57.5	4.8	226	4	US-09-453-234-80	Sequence 80, Appl
887	58	4.8	443	4	US-09-538-092-62	Sequence 62, Appl	960	57.5	4.8	229	4	US-09-902-540-10214	Sequence 10214, A
888	58	4.8	443	4	US-09-540-236-3386	Sequence 3386, Ap	961	57.5	4.8	223	4	US-09-270-767-62302	Sequence 62302, A
889	58	4.8	457	1	US-08-264-101-4	Sequence 4, Appli	962	57.5	4.8	255	4	US-09-328-352-7865	Sequence 7865, Ap
890	58	4.8	457	2	US-08-765-243-4	Sequence 4, Appli	963	57.5	4.8	257	4	US-09-248-796A-21037	Sequence 21037, A
891	58	4.8	457	5	PCT-US95-07295-4	Sequence 4, Appli	964	57.5	4.8	268	4	US-09-270-767-44519	Sequence 44519, A
892	58	4.8	458	1	US-08-112-817C-2	Sequence 2, Appli	965	57.5	4.8	273	4	US-09-328-352-6167	Sequence 6167, Ap
893	58	4.8	458	4	US-09-694-519-5	Sequence 5, Appli	966	57.5	4.8	282	4	US-09-949-016-7084	Sequence 7084, Ap
894	58	4.8	458	4	US-09-694-519-7	Sequence 7, Appli	967	57.5	4.8	284	4	US-09-583-110-3189	Sequence 3189, Ap
895	58	4.8	485	4	US-09-270-767-45701	Sequence 45701, A	968	57.5	4.8	315	4	US-09-949-016-9940	Sequence 9940, Ap
896	58	4.8	491	4	US-10-011-125A-2	Sequence 2, Appli	969	57.5	4.8	333	4	US-09-248-796A-15432	Sequence 15432, A
897	58	4.8	496	3	US-09-082-092-10	Sequence 10, Appl	970	57.5	4.8	335	1	US-08-085-122-13	Sequence 13, Appl
898	58	4.8	496	3	US-09-288-292A-46	Sequence 46, Appl	971	57.5	4.8	335	3	US-08-442-108B-23	Sequence 23, Appl
899	58	4.8	496	4	US-09-885-722A-10	Sequence 10, Appl	972	57.5	4.8	335	4	US-09-134-000C-4450	Sequence 4450, Ap
900	58	4.8	509	4	US-09-489-039A-10350	Sequence 10350, A	973	57.5	4.8	336	4	US-09-902-540-15666	Sequence 15666, A
901	58	4.8	524	4	US-10-101-464A-943	Sequence 943, App	974	57.5	4.8	339	3	US-09-161-241-8	Sequence 8, Appli
902	58	4.8	536	4	US-09-902-540-13091	Sequence 13091, A	975	57.5	4.8	352	4	US-09-479-040-11	Sequence 11, Appl
903	58	4.8	538	4	US-09-248-796A-17632	Sequence 17632, A	976	57.5	4.8	382	4	US-09-880-137-8	Sequence 8, Appli

977	57.5	4.8	384	4	US-09-489-039A-9127	Sequence 9127, Ap	1050	57.5	4.8	600	3	US-09-352-168-23	Sequence 23, Appl
978	57.5	4.8	384	4	US-09-270-767-46691	Sequence 46691, A	1051	57.5	4.8	600	4	US-09-771-045B-23	Sequence 23, Appl
979	57.5	4.8	391	2	US-08-353-476-114	Sequence 114, App	1052	57.5	4.8	600	4	US-09-771-045B-33	Sequence 33, Appl
980	57.5	4.8	391	2	US-09-433-248A-2	Sequence 2, Appl	1053	57.5	4.8	600	4	US-09-771-045B-36	Sequence 36, Appl
981	57.5	4.8	397	3	US-09-433-248A-2	Sequence 2, Appl	1054	57.5	4.8	600	4	US-09-771-045B-38	Sequence 38, Appl
982	57.5	4.8	409	4	US-09-880-137-4	Sequence 4, Appl	1055	57.5	4.8	600	4	US-09-771-045B-47	Sequence 47, Appl
983	57.5	4.8	415	4	US-09-543-681A-6350	Sequence 6350, Ap	1056	57.5	4.8	600	4	US-09-882-694B-21	Sequence 21, Appl
984	57.5	4.8	416	4	US-09-328-352-6640	Sequence 6640, Ap	1057	57.5	4.8	600	4	US-09-882-694B-23	Sequence 23, Appl
985	57.5	4.8	426	4	US-09-252-991A-31959	Sequence 31959, A	1058	57.5	4.8	600	4	US-09-882-694B-25	Sequence 25, Appl
986	57.5	4.8	432	4	US-09-198-452A-41	Sequence 41, Appl	1059	57.5	4.8	600	4	US-09-882-694B-27	Sequence 27, Appl
987	57.5	4.8	435	4	US-09-856-061-2	Sequence 2, Appl	1060	57.5	4.8	600	4	US-09-770-564A-23	Sequence 23, Appl
988	57.5	4.8	445	4	US-09-107-532A-5087	Sequence 5087, Ap	1061	57.5	4.8	635	3	US-09-142-623-1	Sequence 1, Appl
989	57.5	4.8	454	3	US-08-929-329-8	Sequence 8, Appl	1062	57.5	4.8	648	1	US-08-487-890A-109	Sequence 109, App
990	57.5	4.8	458	3	US-09-352-159-9	Sequence 9, Appl	1063	57.5	4.8	648	2	US-08-478-435-109	Sequence 109, App
991	57.5	4.8	458	3	US-09-352-168-9	Sequence 9, Appl	1064	57.5	4.8	648	2	US-08-337-483-109	Sequence 109, App
992	57.5	4.8	458	4	US-09-771-045B-9	Sequence 9, Appl	1065	57.5	4.8	648	2	US-08-478-373-109	Sequence 109, App
993	57.5	4.8	458	4	US-09-770-564A-9	Sequence 9, Appl	1066	57.5	4.8	648	3	US-08-474-671-109	Sequence 109, App
994	57.5	4.8	462	3	US-09-352-159-6	Sequence 6, Appl	1067	57.5	4.8	648	3	US-08-483-577A-109	Sequence 109, App
995	57.5	4.8	462	3	US-09-352-159-6	Sequence 6, Appl	1068	57.5	4.8	648	3	US-08-897-438-109	Sequence 109, App
996	57.5	4.8	462	3	US-09-352-168-6	Sequence 6, Appl	1069	57.5	4.8	648	3	US-08-637-654-109	Sequence 109, App
997	57.5	4.8	462	3	US-09-352-168-8	Sequence 8, Appl	1070	57.5	4.8	648	3	US-08-649-518-109	Sequence 109, App
998	57.5	4.8	462	4	US-09-771-045B-8	Sequence 8, Appl	1071	57.5	4.8	680	3	US-08-761-136-1	Sequence 1, Appl
999	57.5	4.8	462	4	US-09-771-045B-8	Sequence 8, Appl	1072	57.5	4.8	680	4	US-09-576-967-1	Sequence 1, Appl
1000	57.5	4.8	462	4	US-09-882-694B-17	Sequence 17, Appl	1073	57.5	4.8	680	4	US-09-538-092-1165	Sequence 1, Appl
1001	57.5	4.8	462	4	US-09-770-564A-6	Sequence 6, Appl	1074	57.5	4.8	680	4	US-10-219-541-1	Sequence 1, Appl
1002	57.5	4.8	462	4	US-09-770-564A-8	Sequence 8, Appl	1075	57.5	4.8	680	4	US-09-949-016-6637	Sequence 6637, Ap
1003	57.5	4.8	463	3	US-09-352-159-11	Sequence 11, Appl	1076	57.5	4.8	692	3	US-09-352-159-19	Sequence 19, Appl
1004	57.5	4.8	463	3	US-09-352-168-11	Sequence 11, Appl	1077	57.5	4.8	692	3	US-09-352-168-19	Sequence 19, Appl
1005	57.5	4.8	463	4	US-09-771-045B-11	Sequence 11, Appl	1078	57.5	4.8	692	3	US-07-757-342D-6	Sequence 6, Appl
1006	57.5	4.8	463	4	US-09-771-045B-49	Sequence 49, Appl	1079	57.5	4.8	692	4	US-09-461-657B-6	Sequence 6, Appl
1007	57.5	4.8	463	4	US-09-771-045B-51	Sequence 51, Appl	1080	57.5	4.8	692	4	US-09-771-045B-19	Sequence 19, Appl
1008	57.5	4.8	463	4	US-09-771-045B-53	Sequence 53, Appl	1081	57.5	4.8	692	4	US-09-770-564A-19	Sequence 19, Appl
1009	57.5	4.8	463	4	US-09-882-694B-19	Sequence 19, Appl	1082	57.5	4.8	708	4	US-09-107-532A-3930	Sequence 3930, Ap
1010	57.5	4.8	463	4	US-09-770-564A-11	Sequence 11, Appl	1083	57.5	4.8	708	4	US-09-949-016-6638	Sequence 6638, Ap
1011	57.5	4.8	465	3	US-09-801-053-2	Sequence 2, Appl	1084	57.5	4.8	712	4	US-09-949-016-7340	Sequence 7340, Ap
1012	57.5	4.8	465	4	US-09-252-991A-18003	Sequence 18003, A	1085	57.5	4.8	726	3	US-09-949-016-7341	Sequence 7341, Ap
1013	57.5	4.8	465	4	US-10-020-121-2	Sequence 2, Appl	1086	57.5	4.8	726	3	US-09-129-075-4	Sequence 4, Appl
1014	57.5	4.8	465	4	US-09-949-016-10240	Sequence 10240, A	1087	57.5	4.8	726	3	US-09-346-237-3	Sequence 3, Appl
1015	57.5	4.8	466	4	US-09-720-318A-8	Sequence 8, Appl	1088	57.5	4.8	726	3	US-09-346-237-13	Sequence 13, Appl
1016	57.5	4.8	472	3	US-09-108-020-12	Sequence 12, Appl	1089	57.5	4.8	726	4	US-09-544-123-4	Sequence 4, Appl
1017	57.5	4.8	472	3	US-09-685-296-12	Sequence 12, Appl	1090	57.5	4.8	808	1	US-08-471-251A-2	Sequence 2, Appl
1018	57.5	4.8	476	3	US-09-078-173A-2	Sequence 2, Appl	1091	57.5	4.8	826	3	US-09-564-805-2	Sequence 2, Appl
1019	57.5	4.8	476	4	US-10-042-991-2	Sequence 2, Appl	1092	57.5	4.8	826	3	US-09-949-016-7736	Sequence 9736, Ap
1020	57.5	4.8	477	4	US-09-252-991A-17093	Sequence 17093, A	1093	57.5	4.8	829	3	US-09-352-159-33	Sequence 33, Appl
1021	57.5	4.8	480	3	US-09-078-173A-3	Sequence 3, Appl	1094	57.5	4.8	829	3	US-09-352-168-33	Sequence 33, Appl
1022	57.5	4.8	480	3	US-10-042-991-3	Sequence 3, Appl	1095	57.5	4.8	829	4	US-09-770-564A-33	Sequence 33, Appl
1023	57.5	4.8	483	3	US-09-078-173A-4	Sequence 4, Appl	1096	57.5	4.8	842	4	US-09-489-039A-12501	Sequence 12501, A
1024	57.5	4.8	483	4	US-10-042-991-4	Sequence 4, Appl	1097	57.5	4.8	871	4	US-09-252-991A-33057	Sequence 33057, A
1025	57.5	4.8	486	4	US-09-134-000C-4392	Sequence 4392, Ap	1098	57.5	4.8	903	4	US-09-252-991A-17937	Sequence 17937, A
1026	57.5	4.8	487	3	US-09-352-159-21	Sequence 21, Appl	1099	57.5	4.8	991	3	US-09-352-159-27	Sequence 27, Appl
1027	57.5	4.8	487	3	US-09-352-168-21	Sequence 21, Appl	1100	57.5	4.8	991	3	US-09-352-168-27	Sequence 27, Appl
1028	57.5	4.8	487	4	US-09-771-045B-21	Sequence 21, Appl	1101	57.5	4.8	991	4	US-09-771-045B-27	Sequence 27, Appl
1029	57.5	4.8	487	4	US-09-770-564A-21	Sequence 21, Appl	1102	57.5	4.8	991	4	US-09-770-564A-27	Sequence 27, Appl
1030	57.5	4.8	488	3	US-09-078-173A-6	Sequence 6, Appl	1103	57.5	4.8	1000	3	US-09-352-159-25	Sequence 25, Appl
1031	57.5	4.8	488	3	US-09-537-357-38	Sequence 38, Appl	1104	57.5	4.8	1000	3	US-09-352-168-25	Sequence 25, Appl
1032	57.5	4.8	488	4	US-10-042-991-6	Sequence 6, Appl	1105	57.5	4.8	1000	4	US-09-771-045B-25	Sequence 25, Appl
1033	57.5	4.8	511	4	US-09-438-185A-475	Sequence 475, App	1106	57.5	4.8	1000	4	US-09-770-564A-25	Sequence 25, Appl
1034	57.5	4.8	515	2	US-08-007-107-2	Sequence 2, Appl	1107	57.5	4.8	1138	4	US-09-252-991A-20291	Sequence 20291, A
1035	57.5	4.8	515	2	US-09-438-185A-25	Sequence 25, Appl	1108	57.5	4.8	1165	4	US-09-949-016-6874	Sequence 6874, Ap
1036	57.5	4.8	544	3	US-09-352-159-17	Sequence 17, Appl	1109	57.5	4.8	1165	4	US-09-949-016-11392	Sequence 11392, A
1037	57.5	4.8	544	3	US-09-352-168-17	Sequence 17, Appl	1110	57.5	4.8	1196	3	US-09-352-159-31	Sequence 31, Appl
1038	57.5	4.8	544	4	US-09-771-045B-17	Sequence 17, Appl	1111	57.5	4.8	1196	3	US-09-352-168-31	Sequence 31, Appl
1039	57.5	4.8	554	4	US-09-770-564A-17	Sequence 17, Appl	1112	57.5	4.8	1196	4	US-09-771-045B-31	Sequence 31, Appl
1040	57.5	4.8	570	3	US-08-747-221B-54	Sequence 54, Appl	1113	57.5	4.8	1196	4	US-09-770-564A-31	Sequence 31, Appl
1041	57.5	4.8	570	3	US-09-005-051-54	Sequence 54, Appl	1114	57.5	4.8	1205	3	US-09-352-159-29	Sequence 29, Appl
1042	57.5	4.8	570	4	US-09-403-942F-54	Sequence 54, Appl	1115	57.5	4.8	1205	3	US-09-352-168-29	Sequence 29, Appl
1043	57.5	4.8	570	4	US-09-252-991A-20435	Sequence 20435, A	1116	57.5	4.8	1205	4	US-09-771-045B-29	Sequence 29, Appl
1044	57.5	4.8	596	3	US-08-747-221B-25	Sequence 25, Appl	1117	57.5	4.8	1205	4	US-09-770-564A-29	Sequence 29, Appl
1045	57.5	4.8	596	3	US-09-005-051-25	Sequence 25, Appl	1118	57.5	4.8	1245	2	US-08-801-263A-3	Sequence 3, Appl
1046	57.5	4.8	596	4	US-09-403-942F-25	Sequence 25, Appl	1119	57.5	4.8	1245	2	US-08-801-263A-6	Sequence 6, Appl
1047	57.5	4.8	600	3	US-09-352-159-23	Sequence 23, Appl	1120	57.5	4.8	1245	2	US-08-801-263A-10	Sequence 10, Appl
1048	57.5	4.8	600	3	US-09-352-159-36	Sequence 36, Appl	1121	57.5	4.8	1245	3	US-09-102-248-3	Sequence 3, Appl
1049	57.5	4.8	600	3	US-09-352-159-38	Sequence 38, Appl	1122	57.5	4.8	1245	3	US-09-102-248-6	Sequence 6, Appl

1123	57.5	4.8	1245	3	US-09-102-248-10	Sequence 10, Appl	1196	57	4.7	467	4	US-09-949-016-7779	Sequence 7779, Ap
1124	57.5	4.8	1245	4	US-09-367-764-3	Sequence 3, Appl	1197	57	4.7	472	2	US-08-459-346-17	Sequence 17, Appl
1125	57.5	4.8	1245	4	US-09-367-764-6	Sequence 6, Appl	1198	57	4.7	472	2	US-08-889-419-17	Sequence 17, Appl
1126	57.5	4.8	1245	4	US-09-367-764-10	Sequence 10, Appl	1199	57	4.7	472	5	US-08-402-542-17	Sequence 17, Appl
1127	57.5	4.8	1279	4	US-09-489-039A-13602	Sequence 13602, A	1200	57	4.7	472	5	PCT-US93-07189-17	Sequence 17, Appl
1128	57.5	4.8	1543	4	US-09-902-540-15547	Sequence 15547, A	1201	57	4.7	475	4	US-09-543-681A-4638	Sequence 4638, Ap
1129	57.5	4.8	1680	3	US-08-487-283A-2	Sequence 2, Appl	1202	57	4.7	478	4	US-09-786-240-31	Sequence 31, Appl
1130	57.5	4.8	1676	4	US-09-949-016-9777	Sequence 9777, Ap	1203	57	4.7	466	4	US-09-252-991A-25645	Sequence 25645, A
1131	57.5	4.8	7831	4	US-09-902-540-12902	Sequence 12902, A	1204	57	4.7	495	4	US-09-252-991A-24997	Sequence 24997, A
1132	57	4.7	110	3	US-09-060-726A-4	Sequence 4, Appl	1205	57	4.7	466	4	US-09-949-016-6987	Sequence 6987, Ap
1133	57	4.7	110	3	US-09-845-849A-12	Sequence 12, Appl	1206	57	4.7	511	4	US-09-248-796A-16380	Sequence 16380, A
1134	57	4.7	119	4	US-09-489-039A-8804	Sequence 8804, Ap	1207	57	4.7	535	4	US-09-252-991A-31946	Sequence 31946, A
1135	57	4.7	124	2	US-08-341-538A-4	Sequence 4, Appl	1208	57	4.7	538	4	US-09-743-992A-9	Sequence 9, Appl
1136	57	4.7	124	2	US-08-725-518-4	Sequence 4, Appl	1209	57	4.7	553	1	US-08-651-572-2	Sequence 2, Appl
1137	57	4.7	145	4	US-09-248-796A-27788	Sequence 27788, A	1210	57	4.7	553	3	US-09-066-544-2	Sequence 2, Appl
1138	57	4.7	188	4	US-09-949-016-10201	Sequence 10201, A	1211	57	4.7	553	3	US-08-951-086-2	Sequence 2, Appl
1139	57	4.7	192	4	US-09-902-540-9869	Sequence 9869, Ap	1212	57	4.7	353	3	US-09-430-669-2	Sequence 2, Appl
1140	57	4.7	195	4	US-09-489-039A-13054	Sequence 13054, A	1213	57	4.7	555	4	US-09-248-796A-20471	Sequence 20471, A
1141	57	4.7	197	4	US-09-849-602-23	Sequence 23, Appl	1214	57	4.7	559	3	US-09-242-690A-15	Sequence 15, Appl
1142	57	4.7	207	2	US-08-951-822-2	Sequence 2, Appl	1215	57	4.7	559	3	US-09-298-924-6	Sequence 6, Appl
1143	57	4.7	207	2	US-09-173-043-25	Sequence 25, Appl	1216	57	4.7	559	4	US-09-908-855-15	Sequence 15, Appl
1144	57	4.7	207	3	US-09-368-951-2	Sequence 2, Appl	1217	57	4.7	576	4	US-09-949-016-7803	Sequence 7803, Ap
1145	57	4.7	207	3	US-09-417-721-14	Sequence 14, Appl	1218	57	4.7	630	3	US-08-860-091A-2	Sequence 2, Appl
1146	57	4.7	207	4	US-09-229-947-2	Sequence 2, Appl	1219	57	4.7	630	3	US-09-245-323A-6	Sequence 6, Appl
1147	57	4.7	234	4	US-09-658-644-8	Sequence 8, Appl	1220	57	4.7	631	4	US-10-003-392A-18	Sequence 18, Appl
1148	57	4.7	234	4	US-09-472-087-17	Sequence 17, Appl	1221	57	4.7	631	4	US-09-107-532A-6577	Sequence 6577, Ap
1149	57	4.7	234	4	US-09-472-087-69	Sequence 69, Appl	1222	57	4.7	633	4	US-09-489-039A-11853	Sequence 11853, A
1150	57	4.7	235	3	US-08-836-226-6	Sequence 6, Appl	1223	57	4.7	666	1	US-08-083-590A-17	Sequence 17, Appl
1151	57	4.7	251	4	US-09-535-679-6	Sequence 6, Appl	1224	57	4.7	666	2	US-08-346-128-36	Sequence 36, Appl
1152	57	4.7	253	4	US-09-252-991A-32676	Sequence 32676, A	1225	57	4.7	666	3	US-08-532-384-17	Sequence 17, Appl
1153	57	4.7	256	4	US-09-489-039A-8774	Sequence 8774, Ap	1226	57	4.7	682	1	US-07-998-003A-107	Sequence 107, App
1154	57	4.7	258	4	US-09-270-767-32813	Sequence 32813, A	1227	57	4.7	682	1	US-08-453-274B-107	Sequence 107, App
1155	57	4.7	258	4	US-09-270-767-48030	Sequence 48030, A	1228	57	4.7	682	1	US-08-453-695A-107	Sequence 107, App
1156	57	4.7	259	4	US-09-862-631-5	Sequence 5, Appl	1229	57	4.7	682	1	US-08-268-161A-107	Sequence 107, App
1157	57	4.7	263	4	US-09-145-476-580	Sequence 580, App	1230	57	4.7	682	2	US-08-453-702A-107	Sequence 107, App
1158	57	4.7	264	4	US-09-949-016-8312	Sequence 8312, Ap	1231	57	4.7	682	3	US-09-039-639-107	Sequence 107, App
1159	57	4.7	280	4	US-09-107-433-3310	Sequence 3310, Ap	1232	57	4.7	682	5	PCT-US93-12588-107	Sequence 107, App
1160	57	4.7	294	4	US-09-583-110-3579	Sequence 3579, Ap	1233	57	4.7	682	5	PCT-US95-08071-107	Sequence 107, App
1161	57	4.7	295	4	US-09-538-092-607	Sequence 607, App	1234	57	4.7	754	4	US-09-949-016-7766	Sequence 7766, App
1162	57	4.7	303	4	US-09-489-039A-11076	Sequence 11076, A	1235	57	4.7	754	4	US-09-300-008B-2	Sequence 2, Appl
1163	57	4.7	312	4	US-09-489-039A-10591	Sequence 10591, A	1236	57	4.7	758	4	US-09-328-352-4521	Sequence 4521, Ap
1164	57	4.7	319	4	US-09-134-000C-3600	Sequence 3600, Ap	1237	57	4.7	775	4	US-09-949-016-8030	Sequence 8030, Ap
1165	57	4.7	325	4	US-09-198-452A-992	Sequence 992, App	1238	57	4.7	816	6	US-09-949-016-7437	Sequence 7437, App
1166	57	4.7	331	4	US-09-438-185A-922	Sequence 922, App	1239	57	4.7	829	3	US-09-514-599-6	Sequence 6, Appl
1167	57	4.7	338	4	US-09-328-352-7427	Sequence 7427, Ap	1240	57	4.7	829	4	US-09-996-024-6	Sequence 6, Appl
1168	57	4.7	347	4	US-09-710-279-3326	Sequence 3326, Ap	1241	57	4.7	830	4	US-09-064-199-19	Sequence 19, Appl
1169	57	4.7	354	3	US-09-338-907-74	Sequence 74, Appl	1242	57	4.7	836	1	US-07-998-003A-105	Sequence 105, App
1170	57	4.7	354	3	US-09-218-207-74	Sequence 74, Appl	1243	57	4.7	836	1	US-08-453-274B-105	Sequence 105, App
1171	57	4.7	363	4	US-09-800-729-111	Sequence 111, App	1244	57	4.7	836	1	US-08-453-695A-105	Sequence 105, App
1172	57	4.7	365	4	US-09-248-796A-20986	Sequence 20986, A	1245	57	4.7	836	1	US-08-268-161A-105	Sequence 105, App
1173	57	4.7	366	4	US-09-750-580-3	Sequence 3, Appl	1246	57	4.7	836	2	US-08-453-702A-105	Sequence 105, App
1174	57	4.7	366	4	US-09-599-360B-89	Sequence 89, Appl	1247	57	4.7	836	3	US-09-039-639-105	Sequence 105, App
1175	57	4.7	366	4	US-09-800-729-212	Sequence 212, App	1248	57	4.7	836	5	PCT-US93-12588-105	Sequence 105, App
1176	57	4.7	371	3	US-09-134-001C-4502	Sequence 4502, Ap	1249	57	4.7	836	5	PCT-US95-08071-105	Sequence 105, App
1177	57	4.7	388	4	US-09-252-991A-30845	Sequence 30845, A	1250	57	4.7	840	4	US-09-949-016-6569	Sequence 6569, Ap
1178	57	4.7	391	4	US-09-248-796A-20335	Sequence 20335, A	1251	57	4.7	862	3	US-09-346-237-1	Sequence 1, Appl
1179	57	4.7	396	4	US-09-134-000C-4226	Sequence 4226, Ap	1252	57	4.7	873	2	US-08-912-129A-61	Sequence 61, Appl
1180	57	4.7	397	4	US-09-090-044B-9	Sequence 9, Appl	1253	57	4.7	879	1	US-08-072-574-6	Sequence 6, Appl
1181	57	4.7	400	4	US-09-949-016-6685	Sequence 6685, Ap	1254	57	4.7	879	1	US-08-466-270-6	Sequence 6, Appl
1182	57	4.7	406	4	US-09-949-016-10207	Sequence 10207, A	1255	57	4.7	879	3	US-08-367-264-6	Sequence 6, Appl
1183	57	4.7	411	4	US-09-657-013-57	Sequence 57, Appl	1256	57	4.7	879	4	US-09-153-757-6	Sequence 6, Appl
1184	57	4.7	411	4	US-09-949-016-6439	Sequence 6439, Ap	1257	57	4.7	879	4	US-09-459-715-6	Sequence 6, Appl
1185	57	4.7	417	4	US-09-902-540-10931	Sequence 10931, A	1258	57	4.7	885	2	US-08-577-492-33	Sequence 33, Appl
1186	57	4.7	422	3	US-09-109-204-30	Sequence 30, Appl	1259	57	4.7	885	3	US-09-079-630-33	Sequence 33, Appl
1187	57	4.7	422	4	US-09-490-032-30	Sequence 30, Appl	1260	57	4.7	904	1	US-07-998-003A-97	Sequence 97, Appl
1188	57	4.7	422	4	US-09-949-016-6448	Sequence 6448, Ap	1261	57	4.7	904	1	US-08-453-274B-97	Sequence 97, Appl
1189	57	4.7	432	4	US-09-949-016-9787	Sequence 9787, A	1262	57	4.7	904	1	US-08-453-695A-97	Sequence 97, Appl
1190	57	4.7	434	4	US-09-489-039A-11311	Sequence 11311, A	1263	57	4.7	904	1	US-08-268-161A-97	Sequence 97, Appl
1191	57	4.7	446	4	US-09-870-472A-2	Sequence 2, Appl	1264	57	4.7	904	2	US-08-453-702A-97	Sequence 97, Appl
1192	57	4.7	446	4	US-09-870-472A-5	Sequence 5, Appl	1265	57	4.7	904	3	US-09-039-639-97	Sequence 97, Appl
1193	57	4.7	448	4	US-09-949-016-6595	Sequence 6595, Ap	1266	57	4.7	904	5	PCT-US93-12588-97	Sequence 97, Appl
1194	57	4.7	464	4	US-09-949-016-10975	Sequence 10975, A	1267	57	4.7	904	5	PCT-US95-08071-97	Sequence 97, Appl
1195	57	4.7	467	4	US-09-949-016-7778	Sequence 7778, Ap	1268	57	4.7	916	4	US-09-949-016-8291	Sequence 8291, Ap

1269	57	4.7	916	4	US-09-949-016-8292	Sequence 8292, Ap	1342	56.5	4.7	449	3	US-09-293-505-29	Sequence 29, Appl
1270	57	4.7	934	4	US-09-949-016-6242	Sequence 6242, Ap	1343	56.5	4.7	449	4	US-09-060-939A-29	Sequence 6, Appl1
1271	57	4.7	941	4	US-09-949-016-10983	Sequence 10983, A	1344	56.5	4.7	472	4	US-09-720-318A-6	Sequence 1217, A
1272	57	4.7	941	4	US-09-949-016-10984	Sequence 10984, A	1345	56.5	4.7	476	4	US-09-489-039A-12217	Sequence 6, Appl1
1273	57	4.7	941	4	US-09-949-016-10985	Sequence 10985, A	1346	56.5	4.7	500	4	US-09-354-123-6	Sequence 6, Appl1
1274	57	4.7	951	4	US-09-252-991A-23338	Sequence 23338, A	1347	56.5	4.7	511	4	US-09-198-452A-509	Sequence 509, Ap
1275	57	4.7	1062	4	US-09-902-540-16313	Sequence 16313, A	1348	56.5	4.7	523	4	US-09-107-532A-4149	Sequence 4149, Ap
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1277	57	4.7	1130	2	US-08-519-547A-6	Sequence 6, Appl1	1350	56.5	4.7	543	2	US-08-808-931-12	Sequence 12, Appl
1278	57	4.7	1130	4	US-09-064-199-18	Sequence 16, Appl	1351	56.5	4.7	543	3	US-08-808-323-12	Sequence 12, Appl
1279	57	4.7	1207	4	US-09-064-199-16	Sequence 16, Appl	1352	56.5	4.7	543	3	US-09-050-603A-12	Sequence 12, Appl
1280	57	4.7	1225	4	US-09-252-991A-25018	Sequence 25018, A	1353	56.5	4.7	543	3	US-09-102-420B-12	Sequence 12, Appl
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1282	57	4.7	1324	2	US-08-811-897A-56	Sequence 56, Appl	1355	56.5	4.7	543	4	US-09-302-357-6	Sequence 12, Appl
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ALIGNMENTS

RESULT 1
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Sequence 3, Application US/09208718
Patent No. 6063767
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer
APPLICANT: Corley, Neil
APPLICANT: Shah, Purni
TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/208, 718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958, 820
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0379 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
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TYPE: amino acid
STRANDBESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLONE: 3126479
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; Sequence 8, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
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RESULT 3

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; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
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Query Match 97.8%; Score 1177; DB 4; Length 227;

Best Local Similarity 98.6%; Pred. No. 3e-124; Indels 0; Gaps 0;

Matches 218; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1  MGMTRLVTAAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
      1  MGMTRLVTAAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
Db      61  VPDNNYRQKITSWMEPIVKPGAVDGYIILVWDPDAPSPAEPRORFWRHMLVTDIKG 120
      61  VPDNNYRQKITSWMEPIVKPGAVDGYIILVWDPDAPSPAEPRORFWRHMLVTDIKG 120
Qy      121  ADLKKGKIQGGELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
      121  ADLKKGKIQGGELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
Db      121  ADLKKGKIQGGELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
      121  ADLKKGKIQGGELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
Qy      181  LNRFLGEPASTQPMTONYQDSPTLQAPRGASBPBKHKTR 221
      181  LNRFLGEPASTQPMTONYQDSPTLQAPRGASBPBKHKQ 221
Db      181  LNRFLGEPASTQPMTONYQDSPTLQAPRGASBPBKHKQ 221
```

RESULT 4

```
US-09-471-276-8
; Sequence 8, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Maline Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
; OTHER INFORMATION: score 8.5
; OTHER INFORMATION: seq AALLGLMMVVTG/DE
US-09-471-276-8
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Query Match 97.8%; Score 1177; DB 4; Length 227;

Best Local Similarity 98.6%; Pred. No. 3e-124; Indels 0; Gaps 0;

Matches 218; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1  MGMTRLVTAAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
      1  MGMTRLVTAAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
Db      1  MGMTRLVTAAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
```

RESULT 7
US-09-492-308A-8

RESULT 7
US-09-492-308A-8

Sequence 8, Application US/09492308A
Patent No. 6573430
GENERAL INFORMATION:
APPLICANT: Bradley, DJ
Carpenter, R
Coen, ES
TITLE OF INVENTION: Flowering genes
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6573430th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,308A
FILING DATE: 27-Jan-2000
CLASSIFICATION: 435 (Preliminary)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/043,029
FILING DATE: 13-MAR-1998
APPLICATION NUMBER: PCT/GB96/02276
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: GB 9518731.6
FILING DATE: 13-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mary J. Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-492-308A-8
Query Match 18.1%; Score 218.5; DB 4; Length 186;
Best Local Similarity 33.3%; Pred. No. 2e-16;
Matches 53; Conservative 24; Mismatches 65; Indels 17; Gaps 4;
QY 46 LEVRY--PELGNIGCKVVPDCNNYRQKTSWMEPIVKFPGAVDGYTLVWVDPAPSPRA 103
DB 24 LQVKGAGAEVDDELGLKVLPTQVKNRPTSITW-----DGLDPGKLYTLVLDPPAPSRK 76
QY 104 EPRQRFMRHWLVTDIKGADLKKGKIQGQELSAHYQAPSPAHSGFRHRYQPFYVLOGEKYIS 163
DB 77 DPKYEMWHFVLVNNKNNISSGVY---LSDYVSGSPKGTGLHRYVWLVYEGQPLKC 132
QY 164 ----LLPKENKTRGSMKMDRFLNRFHLGSPKASTQFMTO 198
DB 133 DEPLISNRSGDHRGKFKVASFRKKEIELGAPVAGTCYQAE 171
RESULT 8
US-08-403-378B-4
Sequence 4, Application US/08403378B
Patent No. 5759991
GENERAL INFORMATION:
APPLICANT: TOHDOH, NAOKI
APPLICANT: TOJO, SHIN-ICHIRO
APPLICANT: KOJIMA, SHIN-ICHI
APPLICANT: UKI, YASUYUKI
APPLICANT: NISHIHARA, TOSHIO

APPLICANT: FUKUSHIMA, NOBUYUKI
APPLICANT: IRIE, TSUNEMASA
APPLICANT: ONO, KEIICHI
APPLICANT: AGUI, HIDEO
APPLICANT: OJIKI, KOSEI
TITLE OF INVENTION: NEUROTROPHIC PEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,378B
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-124688
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-080398
FILING DATE: 30-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-280590
FILING DATE: 27-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-333241
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-243003
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,043
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,764
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01214
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIGGART, WADDELL, A
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-403-378B-4
Query Match 17.5%; Score 210.5; DB 1; Length 187;
Best Local Similarity 36.3%; Pred. No. 1.6e-15;
Matches 57; Conservative 20; Mismatches 59; Indels 21; Gaps 7;
QY 52 ELGNIGCKVVPDCNNYRQKTSWMEPIVKFPGAVDGYTLVWVDPAPSPRAEPRQRFMR 111
DB 36 ELGKV---LFTQVNNRPSISW-----DGLDPGKLYTLVLDPPAPSRKQPKFREWH 85
QY 112 HWLVTDIKGADLKKGKIQGQELSAHYQAPSPAHSGFRHRYQPFYVLOGEKYIS---LLP 166

Db 86 HFLVNNKNDISSGTV---LSEY-VSGSPKDTGLHRRYVWLYVEQOPINCEPILSN 140
Qy 167 KENKTRGSKMDRFLNRFHLGPEASTQPMQYODS 203
Db 141 KSGDNRGKFKVSEFRKXKYLHAPVAGTCYQAE-WDSS 176

RESULT 9
US-08-403-378B-15
; Sequence 15, Application US/08403378B
; Patent No. 575991
; GENERAL INFORMATION:
; APPLICANT: TOHDOH, NAOKI
; APPLICANT: TOJO, SHIN-ICHIRO
; APPLICANT: KOJIMA, SHIN-ICHI
; APPLICANT: Ueki, YASUYUKI
; APPLICANT: NISHIHARA, TOSHIO
; APPLICANT: FUKUSHIMA, NOBUYUKI
; APPLICANT: ONO, KEIICHI
; APPLICANT: IRIE, TSUNEMASA
; APPLICANT: AGUI, HIDEO
; APPLICANT: OIIRA, KOSEI
; TITLE OF INVENTION: NEUTROPHILIC PEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,378B
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-124688
; FILING DATE: 27-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-080398
; FILING DATE: 30-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-280590
; FILING DATE: 27-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-333241
; FILING DATE: 21-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-243003
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,043
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/873,764
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01214
; FILING DATE: 27-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGART, MADDELL A
; REGISTRATION NUMBER: 24,861
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-403-378B-15

Query Match 17.0%; Score 205; DB 1; Length 187;
Best Local Similarity 33.1%; Pred. No. 6.5e-15;
Matches 50; Conservative 21; Mismatches 62; Indels 18; Gaps 4;

Qy 52 ELGNIGCKVVPDCNNRYOKTSMKEPIVKFPGAVDGYLLVMDPAPSPAEPRQRFWR 111
Db 36 ELGRV---LTPYQVKNRPTSISW-----DGLDSGKLYLVLPDPAPSRKPKYRBMH 85
Qy 112 HMLVTDIKGDILKKKIGQSELISYQAPSPRHSGFHRGYFFVYLOEGKYIS----LLPK 167
Db 86 HFLVNNKNDISSGTV---LSDYVSGSPKGTGLHRRYVWLYVEQDRLKCEPILSNR 141
Qy 168 ENKTRGSKMDRFLNRFHLGPEASTQPMQ 198
Db 142 SGRHGRKFKVASFRKXKYLHAPVAGTCYQAE 172

RESULT 10
US-09-060-726A-2
; Sequence 2, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-060-726A-2

Query Match 13.6%; Score 164; DB 3; Length 175;
Best Local Similarity 36.3%; Pred. No. 2.5e-10;
Matches 41; Conservative 13; Mismatches 43; Indels 16; Gaps 4;

Qy 90 YILVMDPAPSPRAEPRQRFWRHMLVTDIKGADILKKKIGQELISAYQAPSPRHSGFHR 149
Db 65 YTLVMDPDPVSPENPHLRVYLHMLVTDIPAT---TGTTGNELVCYENSPPTA--GIHR 119
Qy 150 YQFFVYLQEGKVISLLPENKTRGSKMD---RFLNRFHLGPEASTQPMQ 198
Db 120 VVFTLFRQLGRQTVYAP-----GMRQNFTRFABIVNLGLFVAVFNQCQ 165

RESULT 11
US-09-845-849A-2
; Sequence 2, Application US/09845849A
; Patent No. 6713663
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, Detlef
; APPLICANT: KARDALISKY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026DVI
; CURRENT APPLICATION NUMBER: US/09/845,849A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 2
;
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
;
US-09-845-849A-2

```

Query Match	13.6%;	Score 164;	DB 4;	Length 175;
Best Local Similarity	36.3%;	Pred. No. 2.5e-10;		
Matches 41;	Conservative 13;	Mismatches 43;	Indels 16;	Gaps 4.

QY 90 YILVWVDPRAIPSRAPRQRFWRHWLVTDIKAGDLKKGKIQGQELSAQAPSPRAHSGFHR 149
| | | | | : | | | | | : | | | | |
DQ 65 YTLVWVDPDVEPSNPPLRLRYLHWLVTDIPT--TGTFGNIVCYENPSPTA--GIHR 119

```

QY      150 YQFVYVYLOEGKXVLSLPKNNKTRGSMQND-----RFLNRFPHIGPEASQFMTO 198
          |::||:|::|||::|
Db      120 VFELFRQLGRQTVAP-----GKRQNTREFAEIIYNIIGLPVAAVFYNCQ 165

```

RESULT 12
US-09-270-767-43926
: Sequence 43926, Application US/09270767

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1 APPLICANT Homburger et al.
2 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
3 FILE REFERENCE: File Reference: 7326-094
4 CURRENT APPLICATION NUMBER: US/09/210,767
5 CURRENT FILING DATE: 1999-03-17
6 NUMBER OF SEQ ID NOS: 62517
7 SOFTWARE: Patentin Ver. 2.0

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OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43926

Query Match	13.4%;	Score 161.5;	DB 4;	length 141;
Best Local Similarity	40.2%;	Pred. No. 3.5e-10;		
Matches	35;	Conservative 17;	Mismatches 30;	Indels 5;
				Gaps 3

Dy 76 EPIYKPGAVDGYI--LWVDPDPAESPRAEPRORFWRHMLVTDIKADLKKGKIQQOEL 133
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 46 QPYSWSG-LEGKSNIULTLMWDPDAPTRQDPKYREILHMWSVNIPESN--ENPSGGHSU 102

QY 134 SAYQAPSPRAHSGFHRYOFFVLYLOEGK 160
 : | | | | | | | |
Db 103 AEYVGSGPKDTGLHRYIFLLYRQENK 129

```

RESULT 13
US-09-248-796A-16385
; Sequence 16385, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 28208
; SEQ. ID NO 16385
; LENGTH: 272
; TYPE: PR1
; ORGANISM: Candida albicans
; US-09-248-796A-16385

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Query Match	13.0%;	Score 157;	DB 4;	Length 272;
Best Local Similarity	29.9%;	Pred. No. 2.8e-09;		
Matches 38;	Conservative 23;	Mismatches 46;	Indels 20;	Gaps 3,

```

QY      90 YILVMWDSDPASRAEPRQFRWRHLVTDLK-----GADLKKGKIQGELS 134
      :|||||:::|||||:|:|:|
Db      142 FILVMTDSDPASNSDKHSEYHLVTDLPLHTKNEDGEPESISHPIDVK---EGRELV 197

```

QY 135 ALYQASPRAHSGFRHYQFFVYLQEGKVISL-LPKEKNKTRSGMKMDFLNRFLHGEPEAST 193

Db 198 PYMGPGPEPKNGKRRYVFLLYKQDPNAGEITAPKGRPKMGLLDYQAVSKDWEKQATNS 257

```
QY      194 QFNTONY 200
        : :: | :
Db      258 KLLSVNF 264
```

RESULT 14
US-09-492-308A-2
; Sequence 2, Application US/09492308A

APPLICANT: Bradley, DJ
 Carpenter, R
 Coen, BS
 TITLE OF INVENTION: Flowering genes
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC
 STREET: 8th Floor, 1100 No. 6533430th Glebe Road
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22201-4714

```

;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Releasee #1.0, Version #1.25 (EPO
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/492.308A

```

PRIOR APPLICATION DATA: US 09/043,029
APPLICATION NUMBER: 13-MAR-1998
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: PCT/GB96/02276
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: GB 9518731.6
FILING DATE: 13-SEP-1995
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-93
TELECOMMUNICATION INFORMATION:

TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

ORGANISM: Antirrhinum majus
 IMMEDIATE SOURCE:
 CLONE: CEN PROTEIN
 SEQUENCE DESCRIPTION: SEQ ID NO: 2
 IS-09-492-308A-2

Query Match 12.3%; Score 148; DB 4; Length 181;
Best Local Similarity 29.1%; Pred. No. 1.6e-08;
Matches 44; Conservative 25; Mismatches 62; Indels 20; Gaps 5;
Qy 60 VVPDCN-----YRKQTSWMEPIYKPGAVDGYIILVWDPDAPRAEPOR 108
Db 31 VIYNSNNSIKHYNGHELFPSAVTS--TPRVEVHGDMRSFPTLIMTDPDVGPSDPYLR 88
Qy 109 FWRHMLVTDIG-ADLKKGKIQGOELSAVQAPSPAHSGFHRQPFVYLQSGKVISLIPK 167
Db 89 EHLHWITVDIPETDSSFGK---BVSISEMPRP--NIGHRFVFLPRQKKRGQAMLS 142
Qy 168 ENKTRGSWMDRFLNRFHIGEPPEASTQPMFQ 198
Db 143 PIVCGRDGFNTRKFTQENELGLPVAAVFNQC 173
RESULT 15
US-09-492-308A-23
; Sequence 23, Application US/09492308A
; Patent No. 6573430
; GENERAL INFORMATION:
; APPLICANT: Bradley, DJ
; Carpenter, R
; Coen, ES
; TITLE OF INVENTION: Flowering genes
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6573430th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492,308A
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: 435 (Preliminary)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/043,029
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: PCT/GB96/02276
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: GB 9518731.6
; FILING DATE: 13-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
; US-09-492-308A-23

Query Match 11.8%; Score 142.5; DB 4; Length 177;
Best Local Similarity 31.0%; Pred. No. 6.6e-08;
Matches 39; Conservative 25; Mismatches 49; Indels 13; Gaps 5;
Qy 76 EPIVFGAVDGYIILVWDPDAPRAEPORFWRHMLVTDIG-ADLKKGKIQGOELIS 134
Db 54 KPRVEIHGGDLRSFILWIDBDVGPSPDFLKEHLHWITVINI PGTTDATEGK---EVV 109

Qy 135 AYQAPSPAHSGFHRQPFVYLQSGK--VISLIPKENKTRGSWMDRFLNRFHIGEPPEAS 192
Db 110 SYELPRPSI--GHRFVFLPRQKKRGQAVIFPNIP-----SRDHFTKRFPAVEYDGLPVAA 163
Qy 193 TQPMFQ 198
Db 164 VFFNAQ 169

Search completed: July 20, 2005, 00:03:13
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: July 19, 2005, 23:58:02 ; Search time 40 Seconds
(without alignments)
536.408 Million cell updates/sec

Title: US-10-036-214-61
Perfect score: 1204
Sequence: 1 MGMTMLVLTALLGLMMVV.....PTLQAPRGRASEPDKTRQR 223

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235.5	19.6	187	2 A36126	23K phosphatidylet
2	234.5	19.5	221	2 T31721	hypothetical prote
3	223	18.5	134	2 PC4214	phosphatidylethano
4	222	18.4	152	2 PC4216	phosphatidylethano
5	218.5	18.1	186	2 S00056	basic cytosolic pr
6	218.5	18.1	186	2 S18358	23K protein - rat
7	210	17.4	114	2 PC4215	phosphatidylethano
8	206	17.1	187	2 S46485	phosphatidylethano
9	205	17.0	187	2 I53745	phosphatidylethano
10	183	15.2	172	2 T27310	hypothetical prote
11	182	15.1	175	2 T52446	FT protein homolog
12	169.5	14.1	262	2 A57391	Tccl-2 protein pre
13	164	13.6	175	2 T52447	FT protein (valida
14	148.5	12.3	175	2 T07877	self-pruning prote
15	148	12.3	181	2 S68507	centriodialis pro
16	147	12.2	175	2 C84674	similar to termina
17	139	11.5	152	2 A44947	16k antigen precu
18	137.5	11.4	177	2 T48411	Terminal flower1 (
19	133	11.0	201	2 S51424	hypothetical prote
20	122.5	10.2	219	2 S18843	TFs1 protein - yea
21	113.5	9.4	197	2 C70519	hypothetical prote
22	113	9.4	151	2 B69134	conserved hypotet
23	113	9.4	215	2 T48789	TFs1 related prote
24	110.5	9.2	154	2 H97860	hypothetical prote
25	106	8.8	171	2 B70408	conserved hypotet
26	105	8.7	198	2 B71072	hypothetical prote
27	101	8.4	122	2 T52448	flowering locus T
28	100	8.3	216	2 B84365	hypothetical prote
29	96.5	8.0	150	2 C86600	hypothetical prote

30	96.5	8.0	150	2 C72024	conserved hypotet
31	95	7.9	169	2 B96018	conserved hypotet
32	95	7.9	183	2 G64786	Ybcl protein - Esc
33	95	7.9	201	2 D70519	probable lppc prot
34	93.5	7.8	157	2 A99226	conserved hypotet
35	93.5	7.8	186	2 C75095	hypothetical prote
36	93	7.7	180	2 C82243	conserved hypotet
37	92	7.6	179	2 T36855	conserved hypotet
38	91.5	7.6	551	2 D69282	glutamy1-cRNA synt
39	89.5	7.4	176	2 H70577	hypothetical prote
40	89.5	7.4	1945	2 T13937	plexin A - fruit f
41	88	7.3	370	2 T26091	hypothetical prote
42	87	7.2	150	2 F81740	conserved hypotet
43	86.5	7.2	150	2 G71477	hypothetical prote
44	85.5	7.1	490	2 A35546	muscarinic acetyl
45	83	6.9	2253	2 T30336	nuclear/mitotic ap
46	82.5	6.9	420	2 T14166	fnud protein - Myc
47	82	6.8	176	2 C87070	conserved hypotet
48	80.5	6.7	287	2 A69462	hypothetical prote
49	79	6.6	1004	2 T38074	hypothetical prote
50	78.5	6.5	162	2 T48152	hypothetical prote
51	78	6.5	390	2 T51197	phosphoadenyl-1-su
52	78	6.5	406	2 S71242	hypothetical prote
53	78	6.5	454	2 C96648	hypothetical prote
54	77.5	6.4	1130	2 T30251	repetin - mouse
55	77	6.4	1622	2 JE0378	DNA (cytosine-5')-
56	76.5	6.4	376	2 AE0921	lipopolysaccharide
57	76.5	6.4	534	2 S70971	bfpd protein - Esc
58	76.5	6.4	1212	2 T13804	shs protein - fru
59	76	6.3	748	2 S24134	endopeptidase 2 (B
60	75.5	6.3	844	2 T05227	hypothetical prote
61	75.5	6.3	1032	2 A11697	alpha-mannosidase
62	75.5	6.3	1050	2 A57134	1-phosphatidylinos
63	75	6.2	710	2 S22673	ferrioxamine recep
64	75	6.2	862	2 T34342	hypothetical prote
65	75	6.2	980	1 S45444	BMI1 protein-bindi
66	75	6.2	1041	2 S55862	probable membrane
67	74.5	6.2	399	2 B82723	carbamoyl-phosphat
68	74.5	6.2	455	2 T33572	hypothetical prote
69	74.5	6.2	1036	2 AG1326	alpha-mannosidase
70	74.5	6.2	2607	2 T31678	beta1ractin synthe
71	74	6.1	319	2 AH1247	hypothetical prote
72	74	6.1	319	2 AD1610	probable dioxyena
73	74	6.1	396	2 S76241	ABC transporter in
74	74	6.1	414	2 AD0645	hypothetical prote
75	73.5	6.1	366	2 D83350	hypothetical prote
76	73.5	6.1	503	2 UC5287	Shp substrate-1 pr
77	73	6.1	314	2 S75995	biphenyl dioxyena
78	73	6.1	458	1 A42409	hypothetical prote
79	73	6.1	547	2 H72311	AMP deaminase (BC
80	73	6.1	747	2 T39444	protein-tyrosine-P
81	73	6.1	1711	1 A55148	hypothetical prote
82	72.5	6.0	547	2 T46366	hypothetical prote
83	72.5	6.0	644	2 T12792	hypothetical prote
84	72.5	6.0	1400	2 T31555	hypothetical prote
85	72	6.0	186	2 D81869	hypothetical outer
86	72	6.0	191	2 D95976	probable periplasm
87	72	6.0	191	2 S40177	Exci protein - Rhi
88	72	6.0	265	2 S00033	histone H1.5 - gar
89	72	6.0	276	2 S75249	esterase gl10992 -
90	72	6.0	299	2 JG0187	foliistatin-relate
91	72	6.0	340	2 G83147	conserved hypotet
92	72	6.0	392	2 B84338	hypothetical prote
93	72	6.0	428	2 D75582	hypothetical prote
94	72	6.0	626	2 S33541	catechol oxidase (
95	72	6.0	630	1 S33539	preproteine translo
96	72	6.0	984	2 D70461	valine-cRNA ligase
97	72	6.0	1104	1 SYBYVT	probable [imported
98	71.5	5.9	258	2 H95326	hypothetical prote
99	71.5	5.9	334	2 B81402	hypothetical prote
100	71.5	5.9	382	2 S40987	hypothetical prote
101	71.5	5.9	392	2 D84130	hypothetical prote
102	71.5	5.9	486	2 B86411	protein F3M18.4 [1

103	71.5	5.9	649	2	T05630	hypothetical prote
104	71.5	5.9	725	2	D81976	probable ferric si
105	71.5	5.9	774	1	QRECF6	iron(III) dicitrat
106	71.5	5.9	1047	2	AFI912	hypothetical prote
107	71	5.9	283	4	FOHUE1	retrovirus-related
108	71	5.9	659	2	A64119	glyx protein (EC 3
109	71	5.9	833	1	S20387	outer membrane pro
110	71	5.9	833	2	T14703	fl capase anchor
111	71	5.9	1004	2	B25039	outer cell wall pr
112	71	5.9	1323	2	T00037	hypothetical prote
113	70.5	5.9	144	2	T38634	40s ribosomal prot
114	70.5	5.9	237	2	E71128	arginase related p
115	70.5	5.9	423	2	B88450	protein P21H11.3 (
116	70.5	5.9	525	2	S24791	nucleocapsid prote
117	70.5	5.9	525	2	A49277	nucleocapsid prote
118	70.5	5.9	532	2	T49873	cathexin homolog -
119	70.5	5.9	830	2	S56940	factor arrest prot
120	70	5.8	306	1	J01395	phosphoribosylamin
121	70	5.8	466	2	A40972	muscarinic acetylch
122	70	5.8	466	2	S44655	ZK353.8 protein -
123	70	5.8	485	2	T03638	hypothetical prote
124	70	5.8	641	2	F82202	hypothetical prote
125	70	5.8	831	2	H81158	Fe(III) dicitrate
126	70	5.8	1395	2	S25997	gene atpa intron 1
127	69.5	5.8	255	2	H71154	probable competent
128	69.5	5.8	336	2	S30972	minor tail protein
129	69.5	5.8	456	2	T48291	transcription regu
130	69.5	5.8	476	2	AH2115	gene N protein - r
131	69.5	5.8	525	2	S47308	catechol oxidase (
132	69.5	5.8	599	2	T07097	AMP deaminase (EC
133	69.5	5.8	747	1	A27366	probable membrane
134	69.5	5.8	780	2	H64830	protein-tyrosine-p
135	69.5	5.8	1284	2	T50993	conserved hypotet
136	69.5	5.8	2029	1	TDFFLK	conserved hypotet
137	69	5.7	106	2	B69048	hypothetical prote
138	69	5.7	235	2	B82836	hypothetical prote
139	69	5.7	297	2	AB2284	hypothetical prote
140	69	5.7	403	2	T49645	late LI 52K protei
141	69	5.7	415	1	WMA052	hypothetical prote
142	69	5.7	539	2	T47404	hypothetical prote
143	69	5.7	780	2	D90753	hypothetical prote
144	69	5.7	834	2	B85617	hypothetical prote
145	69	5.7	834	2	T41568	arginate-like pro
146	69	5.7	892	2	T15195	hypothetical prote
147	69	5.7	1647	2	T49412	hypothetical prote
148	69	5.7	2810	2	T22298	coagulogen - horse
149	68.5	5.7	175	1	WCHCS	translation elonga
150	68.5	5.7	189	2	G82586	NADH dehydrogenase
151	68.5	5.7	224	2	B75388	signal sequence pe
152	68.5	5.7	239	2	C84392	hypothetical prote
153	68.5	5.7	335	2	T39033	probable ribosomal
154	68.5	5.7	502	2	T03019	hypothetical prote
155	68.5	5.7	695	2	G85135	hypothetical prote
156	68.5	5.7	706	2	G71004	hypothetical prote
157	68.5	5.7	754	2	A80614	probable competent
158	68.5	5.7	882	2	C83234	hypothetical prote
159	68.5	5.7	948	2	T26417	hypothetical prote
160	68.5	5.7	4307	2	T20721	hypothetical prote
161	68	5.6	205	2	F83333	enolase-phosphatas
162	68	5.6	229	2	A49101	hypothetical prote
163	68	5.6	391	2	T36739	late LI 52K protei
164	68	5.6	415	1	WMA065	hypothetical prote
165	68	5.6	424	2	T46197	lipoprotein lipase
166	68	5.6	475	1	L1RHUL	lipoprotein lipase
167	68	5.6	475	2	JC4242	endo-1,4-beta-xyla
168	68	5.6	603	2	T00379	zonadhesin - pig
169	68	5.6	1075	2	D70568	heat shock protein
170	68	5.6	1173	2	T31421	conserved hypotet
171	68	5.6	1231	1	A48490	coagulogen II prec
172	68	5.6	2476	2	T34022	
173	67.5	5.6	157	2	CYP277	
174	67.5	5.6	168	2	E70080	
175	67.5	5.6	195	1	B27257	
176	67.5	5.6	204	2	G82589	conserved hypotet
177	67.5	5.6	236	2	AG3072	conserved hypotet
178	67.5	5.6	266	2	B98214	bbsi protein (AP17
179	67.5	5.6	277	2	B64206	hypothetical prote
180	67.5	5.6	291	2	S74948	hypothetical prote
181	67.5	5.6	472	2	S27878	selenium-binding p
182	67.5	5.6	516	2	B85301	hypothetical prote
183	67.5	5.6	532	2	S27373	beta-fructofuranos
184	67.5	5.6	550	2	B50723	probable fumarate
185	67.5	5.6	550	2	B85574	conserved hypotet
186	67.5	5.6	582	2	B81048	conserved hypotet
187	67.5	5.6	585	2	B81827	hypothetical prote
188	67.5	5.6	596	1	S33540	catechol oxidase (
189	67.5	5.6	621	1	YRNC	monophenol monooxy
190	67.5	5.6	706	2	S61717	probable membrane
191	67.5	5.6	1430	2	D82533	RNA polymerase bet
192	67	5.6	41	2	PN0155	RAF-24.5K protein
193	67	5.6	114	2	S04585	neural cell adhesi
194	67	5.6	120	2	A48837	subgroup A Rous sa
195	67	5.6	157	2	B48837	subgroup A Rous sa
196	67	5.6	158	1	QRECB6	conserved hypotet
197	67	5.6	158	2	AF0596	conserved hypotet
198	67	5.6	158	2	D85585	hypothetical prote
199	67	5.6	158	2	C90735	hypothetical prote
200	67	5.6	205	1	S33228	ribosomal protein
201	67	5.6	274	2	D50814	probable beta-gluc
202	67	5.6	274	2	B85673	beta-glucosidase (
203	67	5.6	311	2	C84101	hypothetical prote
204	67	5.6	330	2	G82373	glycyl-tRNA synthe
205	67	5.6	346	2	H72237	hypothetical prote
206	67	5.6	361	2	T21136	hypothetical prote
207	67	5.6	367	2	D82261	phoH family protei
208	67	5.6	372	2	A55262	protein kinase (EC
209	67	5.6	431	2	D75455	tryptophan synthas
210	67	5.6	465	2	B85058	5'-adenylylsulfate
211	67	5.6	474	1	JH0790	lipoprotein lipase
212	67	5.6	505	2	S08598	hypothetical prote
213	67	5.6	543	2	S68467	CD40 receptor-asso
214	67	5.6	556	2	JC5132	alpha-amylase (EC
215	67	5.6	567	2	I49272	CD40 receptor-asso
216	67	5.6	568	2	A55960	CD40 receptor-asso
217	67	5.6	678	2	T43539	sprindie checkpoint
218	67	5.6	793	2	AB1750	exoribonuclease RN
219	67	5.6	812	2	T03659	phospholipase D (E
220	67	5.6	4151	2	G70944	probable polyketid
221	66.5	5.5	309	2	H81993	hypothetical prote
222	66.5	5.5	410	2	A29393	hemocyanin beta-c
223	66.5	5.5	429	2	F86240	hypothetical prote
224	66.5	5.5	495	2	G84193	Glu-tRNA amidotran
225	66.5	5.5	532	2	S27372	beta-fructofuranos
226	66.5	5.5	633	2	T39352	hypothetical prote
227	66.5	5.5	725	2	H72336	maltohextrin glyco
228	66.5	5.5	725	2	H81030	TonB-dependent rec
229	66.5	5.5	790	2	T34293	hypothetical prote
230	66.5	5.5	973	2	T35238	probable secreted
231	66.5	5.5	1948	2	S00485	gene 11-1 protein
232	66.5	5.5	2397	1	A55535	versalbin precursor
233	66	5.5	186	2	F85044	probable M-type th
234	66	5.5	238	2	C70479	thiol-disulfide in
235	66	5.5	311	2	AF2353	hypothetical prote
236	66	5.5	350	2	AE2247	muconate cyclisom
237	66	5.5	401	2	AI2842	carbamoylphosphate
238	66	5.5	423	2	AC1068	probable membrane
239	66	5.5	456	2	B97620	hypothetical prote
240	66	5.5	466	2	T41076	hypothetical prote
241	66	5.5	493	1	D64806	probable proton/ol
242	66	5.5	493	2	P90720	probable transport
243	66	5.5	493	2	B85571	probable transport
244	66	5.5	520	2	AE2750	acyl-CoA dehydroge
245	66	5.5	547	2	B97531	probable acyl-CoA
246	66	5.5	638	2	E71733	threonine-tRNA lig
247	66	5.5	638	2	T36309	probable transcrip
248	66	5.5	692	2	AD1857	hypothetical prote

249	66	5.5	775	2	S67920	DNA-directed DNA p	322	64.5	5.4	258	2	G97655	hypothetical prote
250	66	5.5	776	2	B96666	protein F22C12.6 l	323	64.5	5.4	300	1	NDBPT7	exodeoxyribonuclea
251	66	5.5	795	2	T43447	hypothetical prote	324	64.5	5.4	309	2	E83243	probable transcrip
252	66	5.5	1042	2	S76045	hypothetical prote	325	64.5	5.4	319	2	D90482	dehydrogenase, pro
253	66	5.5	1078	2	D87647	hypothetical prote	326	64.5	5.4	390	2	AF0842	multitrdng resistan
254	66	5.5	1095	2	B83471	probable pyruvate	327	64.5	5.4	396	2	H72224	hypothetical prote
255	66	5.5	1520	2	T30820	carbamoyl-1-phosphat	328	64.5	5.4	407	2	C71055	probable RNA methyl
256	66	5.5	1524	2	T30518	carbamoyl-1-phosphat	329	64.5	5.4	439	2	S25483	ribulose biphosph
257	66	5.5	2089	1	A48757	acetyl-CoA carboxy	330	64.5	5.4	442	2	S20908	tubulin beta chain
258	66	5.5	2325	2	A61208	chondroitin sulfat	331	64.5	5.4	445	2	A60488	histidine-rich gly
259	66	5.5	2478	2	AH2140	polyketide synthas	332	64.5	5.4	447	2	AF1751	RNA polymerase sig
260	66	5.5	3068	1	A44062	genome polypotein	333	64.5	5.4	454	2	S75610	UDP-N-acetylmutramo
261	66	5.5	1222	2	AB0019	probable membrane	334	64.5	5.4	462	2	G82094	sodium-translocati
262	66	5.5	159	1	UN0441	Shaking J neural p	335	64.5	5.4	471	2	AB2266	trigger factor [lm
263	66	5.5	195	1	CYP279	heat shock protein	336	64.5	5.4	512	2	T45686	receptor-like prot
264	66	5.5	266	2	WCHCA	coagulogen precurs	337	64.5	5.4	540	2	S76076	hypothetical prote
265	66	5.5	276	2	T20142	hypothetical prote	338	64.5	5.4	551	2	H72117	methionine-tRNA 11
266	66	5.5	269	2	T47120	pantoate-beta-alan	339	64.5	5.4	558	2	S38614	hypothetical prote
267	66	5.5	282	2	H71547	probable disulfide	340	64.5	5.4	613	2	H82022	glutamine-fructose
268	66	5.5	368	2	G87637	hypothetical prote	341	64.5	5.4	612	2	S48557	hypothetical prote
269	66	5.5	375	2	H90786	hypothetical prote	342	64.5	5.4	617	2	G64972	YegA protein precu
270	66	5.5	375	2	H85646	hypothetical prote	343	64.5	5.4	692	2	C55926	DNA binding protei
271	65.5	5.4	375	2	H64843	ycdo protein - Bsc	344	64.5	5.4	753	2	JC2099	glutenin, high mol
272	65.5	5.4	409	2	H69506	probable acyl-CoA	345	64.5	5.4	786	2	T49414	related to ammp1 p
273	65.5	5.4	423	2	AB3691	hypothetical prote	346	64.5	5.4	812	2	T03402	probable phosphol
274	65.5	5.4	435	2	B86149	TiN6.17 protein -	347	64.5	5.4	830	2	T49270	receptor protein X
275	65.5	5.4	448	2	C83793	hypothetical prote	348	64.5	5.4	1038	1	S03632	lysine-ketoglutar
276	65.5	5.4	456	2	C70481	translacton initia	349	64.5	5.4	1056	2	T02930	alpha-mannosidase-
277	65.5	5.4	459	2	B44498	radial spoke prote	350	64.5	5.4	1176	2	T51440	myosin-light-chain
278	65.5	5.4	469	2	S44620	C50C3.1 protein -	351	64.5	5.4	1176	2	UN0583	myosin-11g-chain
279	65.5	5.4	542	2	I39540	chitinase (EC 3.2.	352	64.5	5.4	1221	2	T52347	disease resistance
280	65.5	5.4	562	2	B70609	hypothetical prote	353	64.5	5.4	12819	2	A90551	conserved hypochet
281	65.5	5.4	664	2	F83376	conserved hypochet	354	64	5.3	200	2	A69212	hypothetical prote
282	65.5	5.4	709	2	B75601	probable transposa	355	64	5.3	263	2	AC0522	probable secreted
283	65.5	5.4	837	2	D69171	intracellular prot	356	64	5.3	385	2	T22822	hypothetical prote
284	65.5	5.4	892	2	HA2736	DNA topoisomerase	357	64	5.3	397	2	F72072	probable transamin
285	65.5	5.4	892	2	F97517	pltrilysin (EC 3.4	358	64	5.3	397	2	C86552	aspartate aminotra
286	65.5	5.4	1265	2	T03302	hypothetical prote	359	64	5.3	442	2	G70158	UDP-N-acetylglucos
287	65.5	5.4	3795	2	T00881	probable sporitit-a	360	64	5.3	445	2	D86620	phosphoshikimate v
288	65	5.4	231	2	B71261	hypothetical prote	361	64	5.3	502	2	C72004	phosphoshikimate v
289	65	5.4	255	2	D70635	hypothetical prote	362	64	5.3	502	2	T35910	probable carboxyle
290	65	5.4	306	2	B51361	follietatic-relate	363	64	5.3	503	2	AB1061	leucyl aminopeptid
291	65	5.4	359	2	B85566	probable ATP-bind1	364	64	5.3	532	2	T46649	1,3-beta-glucan sy
292	65	5.4	359	2	B64801	ybe2 protein - Bsc	365	64	5.3	570	2	T49181	cyclophyljin-like p
293	65	5.4	359	2	B80716	probable ATP-bind1	366	64	5.3	611	2	AC2094	two-component resp
294	65	5.4	389	2	D40785	hypothetical 46k p	367	64	5.3	612	2	C64535	threonine-tRNA lig
295	65	5.4	459	1	B41858	biphenyl dioxygena	368	64	5.3	641	2	S64064	probable membrane
296	65	5.4	559	2	C87307	hypothetical prote	369	64	5.3	645	2	A75390	NMDH2 dehydrogenas
297	65	5.4	614	2	B95668	unknown protein, 1	370	64	5.3	662	2	C97507	hypothetical prote
298	65	5.4	622	2	A40144	prolactin receptor	371	64	5.3	662	2	AG2725	2',3'-cyclic-nucle
299	65	5.4	629	2	T15945	hypothetical prote	372	64	5.3	664	2	G86663	hypothetical prote
300	65	5.4	635	2	H97736	threonine-tRNA lig	373	64	5.3	787	2	C75068	probable beta-gala
301	65	5.4	692	2	T50259	probable serine/th	374	64	5.3	920	2	T26650	hypothetical prote
302	65	5.4	677	2	T00267	hypothetical prote	375	64	5.3	1065	2	A70797	hypothetical prote
303	65	5.4	733	2	T49679	probable branching	376	64	5.3	1146	2	S46837	myosin heavy chain
304	65	5.4	773	2	T46283	hypothetical prote	377	64	5.3	1147	1	MMAX1B	coagulogen I - hor
305	65	5.4	1066	2	F71100	isoleucine-tRNA li	378	63.5	5.3	175	1	WCHCJ	hypothetical prote
306	65	5.4	1087	1	S41797	cellulose 1,4-beta	379	63.5	5.3	231	2	C97552	hypothetical prote
307	65	5.4	1177	2	AD0438	probable exported	380	63.5	5.3	231	2	AD2772	hypothetical prote
308	65	5.4	1284	2	G86145	protein-cyrosine-p	381	63.5	5.3	260	2	AH2158	hypothetical prote
309	65	5.4	1291	1	A28334	transposible eleme	382	63.5	5.3	268	2	S76063	hypothetical prote
310	65	5.4	1308	2	B32494	hypothetical prote	383	63.5	5.3	308	2	T49920	hypothetical prote
311	65	5.4	1352	2	G84473	hypothetical prote	384	63.5	5.3	390	2	F65048	multitrdng resistan
312	65	5.4	1424	2	T03851	thyroid hormone re	385	63.5	5.3	414	2	AH1662	sugar ABC transpor
313	65	5.4	1434	2	T30172	transmembrane prot	386	63.5	5.3	440	2	A56693	receptor protein k
314	65	5.4	2241	2	S09811	hypothetical prote	387	63.5	5.3	482	2	S10180	bacteriocidal perme
315	65	5.4	4116	2	T13719	calo protein - fru	388	63.5	5.3	485	2	T27548	hypothetical prote
316	64.5	5.4	152	1	AS7321	B48 antigen precu	389	63.5	5.3	496	2	AB2219	hypothetical prote
317	64.5	5.4	152	2	T17873	hypothetical prote	390	63.5	5.3	499	2	JC2062	transfoming growt
318	64.5	5.4	212	1	CTSHP	corticocortopin / li	391	63.5	5.3	503	2	AC4432	activin receptor-1
319	64.5	5.4	232	2	B90592	pseudouridylylate sy	392	63.5	5.3	503	2	JC2061	transfoming growt
320	64.5	5.4	253	2	AB1269	conserved hypochet	393	63.5	5.3	525	2	H70982	probable fadD7 pro
321	64.5	5.4	258	2	AE2879		394	63.5	5.3	527	2	T02128	beta-glucosidase h

395	63.5	5.3	597	1	P21VTV	RNA-directed RNA p	468	62.5	5.2	210	2	D87724	protein F37F2.1 [i
396	63.5	5.3	612	2	B81246	glutamine-fructose	469	62.5	5.2	210	2	T33051	hypothetical prote
397	63.5	5.3	663	2	S32825	arachidonate 12-11	470	62.5	5.2	244	2	T12458	hypothetical prote
398	63.5	5.3	732	2	S23001	trial protein - Bac	471	62.5	5.2	261	2	C72128	hypothetical prote
399	63.5	5.3	796	2	G82582	bifunctional penic	472	62.5	5.2	261	2	F86494	hypothetical prote
400	63.5	5.3	831	2	S50163	nitrate reductase	473	62.5	5.2	269	2	AF0138	probable exported
401	63.5	5.3	889	2	H96606	hypothetical prote	474	62.5	5.2	278	2	G81139	hypothetical prote
402	63.5	5.3	909	2	T00009	probable primase (475	62.5	5.2	283	2	T49546	hypothetical prote
403	63.5	5.3	934	2	T08418	protein kinase (BC	476	62.5	5.2	288	2	T04894	hypothetical prote
404	63.5	5.3	945	2	A64714	helicase - Helicob	477	62.5	5.2	295	2	A49906	glucose-1-phosphat
405	63.5	5.3	1192	2	T17255	hypothetical prote	478	62.5	5.2	307	2	T19906	hypothetical prote
406	63.5	5.3	1861	2	T13845	microtubule-associ	479	62.5	5.2	309	1	B51112	hypothetical 34.6
407	63	5.2	140	1	S57774	thioredoxin m prec	480	62.5	5.2	309	2	B85985	hypothetical prote
408	63	5.2	175	2	E90877	probable copper/z1	481	62.5	5.2	309	2	B91140	hypothetical prote
409	63	5.2	246	2	S46747	hypothetical prote	482	62.5	5.2	319	2	B90958	probable plasmid p
410	63	5.2	247	2	T50286	hypothetical prote	483	62.5	5.2	319	2	C85806	probable plasmid p
411	63	5.2	255	2	T00320	hypothetical 24.7K	484	62.5	5.2	328	2	A95011	conserved hypotet
412	63	5.2	267	2	T47288	hypothetical prote	485	62.5	5.2	328	2	D97882	conserved hypotet
413	63	5.2	278	2	D86208	protein F22G5.34 l	486	62.5	5.2	344	2	JX0366	cysteine endopepti
414	63	5.2	328	2	E85842	probable superoxid	487	62.5	5.2	361	1	A61648	translation releas
415	63	5.2	330	2	A72534	hypothetical prote	488	62.5	5.2	361	2	AB2462	hypothetical prote
416	63	5.2	341	2	E83779	iron (III) dicitra	489	62.5	5.2	365	2	B90250	oxidoreductase, pr
417	63	5.2	349	2	AF1714	ribonucleoside-dip	490	62.5	5.2	370	2	T40131	hypothetical prote
418	63	5.2	350	2	AC2375	hypothetical prote	491	62.5	5.2	376	2	AC0470	hypothetical prote
419	63	5.2	355	2	AT2867	endo-1,4-beta-xyla	492	62.5	5.2	389	2	AT2230	mannose-1-phosphat
420	63	5.2	365	2	E97644	endo-1,4-beta-xyla	493	62.5	5.2	390	2	F85916	multidrug resistanc
421	63	5.2	426	2	S44953	lmbf protein - Str	494	62.5	5.2	390	2	C91072	multidrug resistanc
422	63	5.2	435	2	S52203	vsf-1 protein - to	495	62.5	5.2	414	2	AB1291	sugar ABC transpor
423	63	5.2	464	2	T38356	sepin homolog spn	496	62.5	5.2	445	2	T49556	epithelial zinc-fi
424	63	5.2	474	2	S77650	probable transpasa	497	62.5	5.2	464	2	C84686	probable Ap2 domai
425	63	5.2	478	1	S60754	transcription fact	498	62.5	5.2	504	1	A32985	cytochrome P450 4A
426	63	5.2	478	2	S18158	lipoprotein lipase	499	62.5	5.2	506	2	H70928	hypothetical prote
427	63	5.2	527	2	G85760	hypothetical prote	500	62.5	5.2	522	2	F70143	hypothetical prote
428	63	5.2	527	2	H90858	hypothetical prote	501	62.5	5.2	537	2	T04745	hypothetical prote
429	63	5.2	529	2	T35831	probable D-3-phosp	502	62.5	5.2	558	2	A13394	metal dependent hy
430	63	5.2	529	2	G82759	hypothetical prote	503	62.5	5.2	559	2	G89931	DNA repair protein
431	63	5.2	530	2	JN0597	calnexin-like prot	504	62.5	5.2	586	2	B84271	glutamyl-tRNA synt
432	63	5.2	532	1	IFBY	beta-fructofuranos	505	62.5	5.2	589	2	F86202	hypothetical prote
433	63	5.2	545	2	T02079	probable carbonate	506	62.5	5.2	602	2	G83388	probable binding p
434	63	5.2	549	2	S04845	Ig heavy chain pre	507	62.5	5.2	607	2	E84889	hypothetical prote
435	63	5.2	582	2	S57722	sl1-1 protein - Ca	508	62.5	5.2	606	2	E71518	probable lipid A d
436	63	5.2	589	2	E97376	sulfite reductase	509	62.5	5.2	616	2	A30304	prolactin receptor
437	63	5.2	589	2	AD2594	hypothetical prote	510	62.5	5.2	637	2	A45777	cell division cont
438	63	5.2	606	2	AF2903	GTP-binding cyrosi	511	62.5	5.2	688	2	S65241	hypothetical prote
439	63	5.2	606	2	H97678	hypothetical prote	512	62.5	5.2	844	2	T37690	hypothetical prote
440	63	5.2	612	2	G71972	cheomone-cRNA lig	513	62.5	5.2	858	2	S68227	ubiquitin thiolest
441	63	5.2	616	2	T38717	probable GTP-bind	514	62.5	5.2	898	2	F97993	phosphoenolpyruvat
442	63	5.2	629	2	T19563	hypothetical prote	515	62.5	5.2	905	2	T00475	probable disease r
443	63	5.2	644	2	S65302	hypothetical prote	516	62.5	5.2	1043	2	T43502	1-phosphatidylinos
444	63	5.2	648	2	AB3792	acetyl-CoA synthet	517	62.5	5.2	1068	1	JQ1329	sucrose-phosphat
445	63	5.2	651	2	T40459	hypothetical lysin	518	62.5	5.2	1115	1	IJMSNL	neural cell adhesi
446	63	5.2	657	2	A54278	DNA-binding protei	519	62.5	5.2	1254	1	S46636	hypothetical prote
447	63	5.2	683	2	A39784	phycobiosome anch	520	62.5	5.2	1276	2	T09204	probable tail-host
448	63	5.2	738	2	C84700	hypothetical prote	521	62.5	5.2	1291	2	T09204	probable tail-host
449	63	5.2	748	1	S74389	phytochrome phy	522	62.5	5.2	1551	1	A43364	M polypeptide prec
450	63	5.2	753	2	AE0187	probable iron-side	523	62.5	5.2	1554	2	C72647	hypothetical prote
451	63	5.2	778	2	B71164	probable beta-gala	524	62.5	5.2	1603	1	BVAS41	3-dehydroquinat
452	63	5.2	966	2	D96662	hypothetical prote	525	62.5	5.2	2215	2	T16871	hypothetical prote
453	63	5.2	1004	2	JH0470	Na+/K+-exchanging	526	62.5	5.2	2352	2	C83229	conserved non-ribos
454	63	5.2	1085	2	S40476	Ca(2+)-sensing rec	527	62	5.1	2352	2	F83483	conserved hypotet
455	63	5.2	1223	2	S43579	C28A5.1 protein (C	528	62	5.1	165	2	B97317	uncharacterized co
456	63	5.2	1274	2	B81779	proline dehydrogen	529	62	5.1	182	2	D56350	Ce-tbx-2 protein -
457	63	5.2	1438	2	A10093	patched hypotet	530	62	5.1	196	2	D85024	P II nitrogen sens
458	63	5.2	1442	2	T18538	conserved hypotet	531	62	5.1	241	2	C70549	hypothetical prote
459	63	5.2	1676	2	A56508	annuleate primary	532	62	5.1	250	2	D75364	hypothetical prote
460	63	5.2	4450	1	JX0340	gramicidin S synth	533	62	5.1	261	2	JC5284	hypothetical prote
461	63	5.2	4452	1	YG8SG2	gramicidin S synth	534	62	5.1	277	2	T05284	carboxyl reductase
462	62.5	5.2	133	2	AG3048	conserved hypotet	535	62	5.1	284	2	T00809	probable esterase
463	62.5	5.2	149	2	D98237	hypothetical prote	536	62	5.1	284	2	AB0521	AMPe protein (limp
464	62.5	5.2	149	2	T04171	heat shock protein	537	62	5.1	301	2	A70039	ABC transporter (A
465	62.5	5.2	156	2	S71566	heat shock protein	538	62	5.1	303	2	S75554	tRNA delta-2-isope
466	62.5	5.2	205	2	AD0788	heme exporter prot	539	62	5.1	306	2	A48993	protein-tyrosine-p
467	62.5	5.2	205	2	AC0960	heme exporter prot	540	62	5.1	314	2	T45077	ornithine carbanoy

541	62	5.1	318	2	A86750	hypothetical prote
542	62	5.1	321	2	A12679	conserved hypotet
543	62	5.1	321	2	G97461	hypothetical prote
544	62	5.1	332	2	T02031	1,3-beta-glucanase
545	62	5.1	334	2	A82443	D-alanine-D-alanin
546	62	5.1	346	2	S72222	ferredoxin-NADP re
547	62	5.1	349	2	AB1344	ribonucleoside-dip
548	62	5.1	352	2	AC1943	periplasmic phosph
549	62	5.1	352	2	S76078	streptogramin lyas
550	62	5.1	361	2	AB0584	phoH-like Arp-bind
551	62	5.1	368	2	AC2840	ABC transporter, s
552	62	5.1	368	2	B37617	hypothetical prote
553	62	5.1	381	2	B87470	hypothetical prote
554	62	5.1	405	2	A35620	coenzyme F420 hydr
555	62	5.1	412	2	I46421	thymoxime-binding
556	62	5.1	436	2	JC1497	alpha-amino-epsilo
557	62	5.1	440	2	T20092	hypothetical prote
558	62	5.1	456	2	B55239	phosphomannomutase
559	62	5.1	456	2	C90983	phosphomannomutase
560	62	5.1	456	2	F85828	phosphomannomutase
561	62	5.1	460	2	S09508	muscarinic acetylch
562	62	5.1	487	2	AI1146	hypothetical cell
563	62	5.1	491	2	T16691	hypothetical prote
564	62	5.1	503	2	AP2029	regulatory protein
565	62	5.1	504	2	S17248	SHP substrate-1 pr
566	62	5.1	509	2	JC5288	periplasmic glucan
567	62	5.1	511	2	AG0636	hypothetical prote
568	62	5.1	513	2	B96524	hypothetical prote
569	62	5.1	521	2	T27996	hypothetical prote
570	62	5.1	542	2	B86628	prophage psi prote
571	62	5.1	551	2	C86506	methionyl-tRNA syn
572	62	5.1	551	2	H81552	methionyl-tRNA syn
573	62	5.1	573	2	AB0611	transport Arp-bind
574	62	5.1	588	2	T48766	probable sugar tra
575	62	5.1	600	2	T01259	AMP deaminase homo
576	62	5.1	640	2	S75175	hypothetical prote
577	62	5.1	650	2	AB2004	hypothetical prote
578	62	5.1	710	2	B83360	conserved hypotet
579	62	5.1	756	2	S40305	multicystatin - po
580	62	5.1	798	2	I50479	neurofilament medi
581	62	5.1	822	2	F86812	phosphoketolase [i
582	62	5.1	849	1	UPVAD	noncapsid protein
583	62	5.1	962	2	T51924	dat-18 protein - C
584	62	5.1	965	2	T32574	hypothetical prote
585	62	5.1	1021	2	T08601	hypothetical prote
586	62	5.1	1063	2	B96662	hypothetical prote
587	62	5.1	1130	1	TVHUA	protein-tyrosine k
588	62	5.1	1199	2	T47442	disease resistance
589	62	5.1	1221	2	T23472	hypothetical prote
590	62	5.1	1228	2	T18897	hypothetical prote
591	62	5.1	1276	2	F83086	hypothetical prote
592	62	5.1	1335	2	U01258	RNA-directed RNA p
593	62	5.1	1413	2	D88844	protein 2K792.1 [i
594	62	5.1	1701	2	T09127	probable erythrocy
595	62	5.1	1816	2	F83901	hypothetical prote
596	62	5.1	1956	2	T00051	hypothetical prote
597	62	5.1	2039	2	T15347	anhydrin-related un
598	62	5.1	2039	2	A54794	dynein heavy chain
599	62	5.1	1444	1	AC2130	hypothetical prote
600	61.5	5.1	188	2	B97104	phospholipase D fa
601	61.5	5.1	194	2	G81726	conserved hypotet
602	61.5	5.1	215	2	S30169	aluminum-lyase
603	61.5	5.1	228	2	D90626	cytochrome c oxida
604	61.5	5.1	243	2	B82979	hypothetical prote
605	61.5	5.1	270	2	B64561	DNA processing cha
606	61.5	5.1	272	2	C75291	guanylate kinase -
607	61.5	5.1	285	2	AC2047	hypothetical prote
608	61.5	5.1	282	2	T22722	hypothetical prote
609	61.5	5.1	299	2	F87415	glycyl-tRNA synthe
610	61.5	5.1	321	2	T07043	probable epoxide h
611	61.5	5.1	322	2	B96014	probable sugar upt
612	61.5	5.1	356	2	G86078	fiv operon protein
613	61.5	5.1	356	2	H91231	fiv operon protein
614	61.5	5.1	362	2	E83542	hypothetical prote
615	61.5	5.1	405	2	C90194	hypothetical prote
616	61.5	5.1	453	2	D40630	phosphomannomutase
617	61.5	5.1	469	2	B81050	hypothetical prote
618	61.5	5.1	469	2	B81826	probable integral
619	61.5	5.1	490	2	F87443	conserved hypotet
620	61.5	5.1	505	2	S76722	UDP-N-acetylmuramo
621	61.5	5.1	507	2	T20293	hypothetical prote
622	61.5	5.1	520	2	S72324	ocotate reductase
623	61.5	5.1	535	2	AE3202	hypothetical prote
624	61.5	5.1	544	2	AP2248	hypothetical prote
625	61.5	5.1	561	2	JE0158	dwarf protein, OSD
626	61.5	5.1	563	2	B82579	peptidase synthase X
627	61.5	5.1	566	2	T15866	hypothetical prote
628	61.5	5.1	577	2	AE1697	two-component sens
629	61.5	5.1	578	2	AG0119	probable OmpA-fam1
630	61.5	5.1	660	1	ALBS	alpha-amylase (EC
631	61.5	5.1	672	2	E81242	conserved hypotet
632	61.5	5.1	693	2	C83821	glycyl-tRNA synthe
633	61.5	5.1	699	2	A70300	translational elonga
634	61.5	5.1	728	2	D86233	hypothetical prote
635	61.5	5.1	775	2	S35543	DNA-directed DNA p
636	61.5	5.1	822	2	S56823	probable membrane
637	61.5	5.1	858	2	S30571	DNA topoisomerase
638	61.5	5.1	864	2	T42556	tegument protein 1
639	61.5	5.1	872	1	TNBERH	97K alpha trans-in
640	61.5	5.1	883	2	AE0207	conserved hypotet
641	61.5	5.1	902	2	C83964	cation-transportin
642	61.5	5.1	906	2	T28034	hypothetical prote
643	61.5	5.1	959	1	B71405	probable kinesin -
644	61.5	5.1	1034	2	T17458	chromosome condens
645	61.5	5.1	1040	1	A38306	alpha-mannosidase
646	61.5	5.1	1062	2	T46444	hypothetical prote
647	61.5	5.1	1842	2	T43409	probable fatty-aci
648	61.5	5.1	1842	2	T38781	fatty acid synthas
649	61.5	5.1	2077	1	WZBE24	240K tegument prot
650	61.5	5.1	2078	2	T09326	tegument protein -
651	61.5	5.1	2123	2	S55089	probable acetyl-Co
652	61.5	5.1	2290	1	GNNYE	genome polyprotein
653	61.5	5.1	2549	2	S45340	FKBP-rapamycin-ass
654	61.5	5.1	2643	2	T29149	hypothetical prote
655	61.5	5.1	4848	2	T30289	pristinamycin I sy
656	61.5	5.1	118	1	HRTHM	myohemermythrin [va
657	61.5	5.1	159	2	S72544	heat shock protein
658	61.5	5.1	161	2	E98102	hypothetical prote
659	61.5	5.1	161	2	D95238	PTS system, IIA co
660	61.5	5.1	171	2	E89865	conserved hypotet
661	61.5	5.1	183	2	B64547	hypothetical prote
662	61.5	5.1	183	2	A71962	hypothetical prote
663	61.5	5.1	205	2	T34724	probable membrane
664	61.5	5.1	236	2	B90086	hypothetical prote
665	61.5	5.1	244	2	JE0170	dnaf heat shock pr
666	61.5	5.1	247	2	H69493	phosphoesterase-re
667	61.5	5.1	261	2	J00319	hypothetical 27K p
668	61.5	5.1	281	2	G75430	pentate-beta-alan
669	61.5	5.1	284	2	T29001	hypothetical prote
670	61.5	5.1	286	2	T04268	hypothetical prote
671	61.5	5.1	296	2	D88969	protein FlsH1.9 (
672	61.5	5.1	297	2	H90601	DNA polymerase I (
673	61.5	5.1	297	2	B86161	Flt003.14 protein -
674	61.5	5.1	299	2	AE11208	metal binding prot
675	61.5	5.1	301	2	F83653	oligopeptide ABC t
676	61.5	5.1	303	2	B83164	hypothetical prote
677	61.5	5.1	333	2	A75365	conserved hypotet
678	61.5	5.1	341	2	S37438	transposase - Stre
679	61.5	5.1	351	1	MNXRRW	nonstructural prot
680	61.5	5.1	355	2	I51157	major histocompati
681	61.5	5.1	370	2	AG0319	conserved hypotet
682	61.5	5.1	381	2	B86175	protein FlsP19.21
683	61.5	5.1	385	2	C87250	dnaf protein [impo
684	61.5	5.1	393	2	S59383	probable membrane
685	61.5	5.1	414	2	H90905	probable exonuclea
686	61.5	5.1	414	2	G85711	probable exonuclea

833	60	5.0	274	2	G64854	ycfn protein - Bac
834	60	5.0	281	1	ZBBE12	30.2K zinc-binding
835	60	5.0	306	2	S38251	follietatin-relate
836	5.0	308	2	G98150	dipeptide transpor	
837	60	5.0	315	2	T51683	mpb-related transc
838	60	5.0	328	2	A46521	52K phosphoprotein
839	60	5.0	329	2	S55489	probable galactosy
840	60	5.0	329	2	A91111	hypothetical prote
841	60	5.0	329	2	D85956	hypothetical prote
842	60	5.0	330	2	G90734	hypothetical prote
843	60	5.0	330	2	A85585	unknown protein en
844	60	5.0	330	2	I57835	lymphocyte-specific
845	60	5.0	337	2	T07140	glucan endo-1,3-be
846	60	5.0	357	2	AC3645	flagellar p-ring p
847	60	5.0	362	2	S48270	hypothetical prote
848	60	5.0	365	2	G72306	conserved hypotet
849	60	5.0	371	2	T06382	Knox protein 1 - 9
850	60	5.0	374	2	UC7091	centaurin alpha 1
851	60	5.0	399	2	JC4592	transcription fact
852	60	5.0	399	2	T09375	hypothetical prote
853	60	5.0	408	2	B84591	hypothetical prote
854	60	5.0	421	2	B81843	conserved hypotet
855	60	5.0	421	2	D81098	gcpB protein NMB13
856	60	5.0	422	2	AH3317	phosphoribosylamln
857	60	5.0	422	2	G87188	probable phosphono
858	60	5.0	424	2	B95964	probable MYB famli
859	60	5.0	427	2	A84667	probable cobyrinic
860	60	5.0	435	2	T03545	separatase-cRNA lig
861	60	5.0	437	2	A69128	hypothetical prote
862	60	5.0	443	2	F90213	hypothetical prote
863	60	5.0	448	2	AF1942	GA-binding protein
864	60	5.0	454	1	A40858	hypothetical prote
865	60	5.0	454	2	D69177	probable sulfate a
866	60	5.0	459	2	T08594	muscarinic acetylC
867	60	5.0	460	2	A24325	L-seeryl-CRNasec se
868	60	5.0	463	2	C86034	L-seeryl-CRNasec se
869	60	5.0	463	2	D91187	L-seeryl-CRNasec se
870	60	5.0	463	2	A65159	L-seeryl-CRNasec se
871	60	5.0	483	2	A11908	hypothetical prote
872	60	5.0	486	2	A64909	probable fructuron
873	60	5.0	486	2	E86130	D-mannosate oxidore
874	60	5.0	486	2	B91289	mannonate oxidore
875	60	5.0	486	2	H85719	probable oxidoredu
876	60	5.0	486	2	G30897	probable phosphon
877	60	5.0	492	2	H72473	conserved hypotet
878	60	5.0	493	2	A80703	leucyl aminopeptid
879	60	5.0	503	1	APECA	aminopeptidase A/I
880	60	5.0	503	2	E91283	aminopeptidase A/I
881	60	5.0	503	2	G86124	hypothetical prote
882	60	5.0	507	2	S74641	hypothetical prote
883	60	5.0	513	2	JC5289	SHP substrate-1 pr
884	60	5.0	513	2	F70776	hypothetical prote
885	60	5.0	513	2	T05210	hypothetical prote
886	60	5.0	514	2	B95885	hypothetical prote
887	60	5.0	546	2	B85398	hypothetical prote
888	60	5.0	563	2	S22837	probable membrane
889	60	5.0	568	2	H64879	probable membrane
890	60	5.0	643	2	H83873	ATP-dependent heli
891	60	5.0	658	2	D69431	methionine-tRNA li
892	60	5.0	670	2	F84540	hypothetical prote
893	60	5.0	691	2	B87383	cell cycle histidi
894	60	5.0	726	1	P21VBC	RNA-directed RNA p
895	60	5.0	726	1	P21VBW	RNA-directed RNA p
896	60	5.0	740	2	G95153	neutraminidase, pro
897	60	5.0	744	2	A82822	NAOH-ubiquitnone ox
898	60	5.0	805	2	B97717	viRbA protein prec
899	60	5.0	805	2	T34212	hypothetical prote
900	60	5.0	835	2	F90260	hypothetical prote
901	60	5.0	886	2	A54442	3',5'-cyclic-nucle
902	60	5.0	925	2	T23388	hypothetical prote
903	60	5.0	1141	2	T20611	hypothetical prote
904	60	5.0	1193	2	A86193	hypothetical prote
905	60	5.0	1201	2	F81202	proline dehydrogen
906	60	5.0	1254	2	T41262	mnts family DNA m
907	60	5.0	1261	2	T11365	mutator 2 - fruit
908	60	5.0	1312	2	S68593	DNA-directed DNA p
909	60	5.0	1438	2	S59792	probable membrane
910	60	5.0	1641	2	I38614	helicase II - huma
911	60	5.0	1819	2	T32008	hypothetical prote
912	60	5.0	1927	2	T25604	hypothetical prote
913	60	5.0	1997	1	S12050	protein-tyrosine-p
914	60	5.0	2183	2	T42764	coagulation factor
915	60	5.0	2264	1	GNVWTR	genome polypotein
916	60	5.0	2427	2	T16613	hypothetical prote
917	60	5.0	3149	1	Q08B8	BEF1 protein - hu
918	60	5.0	3570	2	T45025	mucin MUC5B, trach
919	60	5.0	3588	2	I40485	surfactin syntheta
920	60	5.0	4533	1	A53102	alpha-2-macroglobu
921	59.5	4.9	89	2	F90816	probable excisiona
922	59.5	4.9	92	2	B85676	probable excisiona
923	59.5	4.9	94	2	D71284	hypothetical prote
924	59.5	4.9	156	2	JQ1377	18K membrane prote
925	59.5	4.9	172	2	G72327	hypothetical prote
926	59.5	4.9	213	2	T03931	DNA binding protei
927	59.5	4.9	226	2	B85080	hypothetical prote
928	59.5	4.9	262	2	D71557	hypothetical prote
929	59.5	4.9	290	2	A64693	fructose-1,6-bisph
930	59.5	4.9	293	2	S61983	regulatory protein
931	59.5	4.9	307	2	D70741	hypothetical prote
932	59.5	4.9	318	1	YXSAT3	thymidylate syntha
933	59.5	4.9	320	2	T24509	hypothetical prote
934	59.5	4.9	320	2	T36823	probable integral
935	59.5	4.9	338	2	JB0196	hydroxysteroid sul
936	59.5	4.9	342	2	AF2823	hypothetical prote
937	59.5	4.9	342	2	B97601	acta [imported] -
938	59.5	4.9	353	2	T01978	hypothetical prote
939	59.5	4.9	355	2	B87473	acyl-CoA dehydroge
940	59.5	4.9	385	2	E95847	conserved hypotet
941	59.5	4.9	393	2	S57050	cyclophilin-like p
942	59.5	4.9	409	2	T42414	conserved hypotet
943	59.5	4.9	413	2	H88481	protein let-756 [i
944	59.5	4.9	414	2	S55865	probable membrane
945	59.5	4.9	418	2	H83843	L-rhamnose isomera
946	59.5	4.9	422	2	E83083	probable two-compo
947	59.5	4.9	441	2	T43544	sat1 protein - E18
948	59.5	4.9	447	2	AE1382	RNA polymerase sig
949	59.5	4.9	452	2	B84483	hypothetical prote
950	59.5	4.9	461	2	E84474	hypothetical prote
951	59.5	4.9	467	2	AP1317	ATP-dependent DNA
952	59.5	4.9	476	2	S64953	hypothetical prote
953	59.5	4.9	479	1	A42241	glycine hydroxymet
954	59.5	4.9	499	2	F69136	hypothetical prote
955	59.5	4.9	502	2	F84455	probable ribonucle
956	59.5	4.9	516	2	D64207	glutamic acid spec
957	59.5	4.9	516	2	T40584	probable involveme
958	59.5	4.9	520	1	O4BOM	cholesterol monoox
959	59.5	4.9	524	2	JC7594	cytochrome P450 en
960	59.5	4.9	524	2	JC7598	cytochrome P450 en
961	59.5	4.9	525	2	S15207	methane monooxygen
962	59.5	4.9	530	2	T20360	hypothetical prote
963	59.5	4.9	550	2	T39942	Salip - fission ye
964	59.5	4.9	564	2	F87305	alkaline phosphata
965	59.5	4.9	571	2	G75165	glutamy1-tRNA synt
966	59.5	4.9	571	2	T20359	hypothetical prote
967	59.5	4.9	580	2	AB0994	gamma-glutamyltran
968	59.5	4.9	580	2	T51880	hypothetical prote
969	59.5	4.9	608	2	E90374	hypothetical prote
970	59.5	4.9	619	2	S30780	hexose metabolism-
971	59.5	4.9	630	2	S29796	hypothetical prote
972	59.5	4.9	638	2	S12136	somaotrofin recep
973	59.5	4.9	654	2	AB3553	membrane protein r
974	59.5	4.9	662	1	A31349	arachidonate 15-11
975	59.5	4.9	679	2	T50445	conserved hypotet
976	59.5	4.9	697	2	T26707	hypothetical prote
977	59.5	4.9	715	2	S38051	DOAI protein - yea
978	59.5	4.9	716	2	G44490	retrovirus-related

979	59.5	4.9	769	2	F81415	DNA topoisomerase	1052	59	4.9	474	2	S75464	hypothetical prote
980	59.5	4.9	780	2	T35268	probable transcript	1053	59	4.9	475	2	E70972	probable amidase -
981	59.5	4.9	789	2	A30843	glutennin high mole	1054	59	4.9	476	1	UC6505	ectomelysin 2 (EC
982	59.5	4.9	791	2	UN0690	glutennin, high-mol	1055	59	4.9	478	2	T34091	hypothetical prote
983	59.5	4.9	824	2	AD3098	periplasmic nitrat	1056	59	4.9	485	2	C75460	hypothetical prote
984	59.5	4.9	833	2	S62136	CW41 protein - Ye	1057	59	4.9	487	2	A11505	hypothetical cell
985	59.5	4.9	834	2	E98188	periplasmic nitrat	1058	59	4.9	493	2	AB0588	PR2-family transp
986	59.5	4.9	851	2	S50670	BC22 protein - yea	1059	59	4.9	495	2	T13025	hypothetical prote
987	59.5	4.9	876	2	T05943	probable lipoxigen	1060	59	4.9	506	2	A10798	probable membrane
988	59.5	4.9	876	2	F97688	leucyl-tRNA synthet	1061	59	4.9	514	2	C64154	hypothetical prote
989	59.5	4.9	876	2	AC2914	leucyl-tRNA synthet	1062	59	4.9	540	2	A95264	probable ABC trans
990	59.5	4.9	900	2	A95340	cation transport p	1063	59	4.9	544	2	S58532	matk protein (trnk
991	59.5	4.9	902	2	B84652	hypothetical prote	1064	59	4.9	547	2	T39593	exea protein - Aer
992	59.5	4.9	902	2	B84652	probable leucyl tr	1065	59	4.9	549	1	B64557	dipeptide ABC tran
993	59.5	4.9	902	2	B84652	catbamoyl-phosphat	1066	59	4.9	552	1	S35703	colony-stimulating
994	59.5	4.9	1075	2	AB0510	hypothetical prote	1067	59	4.9	552	1	A141401	macrophage colony-
995	59.5	4.9	1087	2	T33759	protein kinase - f	1068	59	4.9	555	2	F69312	heterodisulfide re
996	59.5	4.9	1087	2	S58147	hypothetical prote	1069	59	4.9	555	2	H67672	hypothetical prote
997	59.5	4.9	1139	2	B70954	hypothetical prote	1070	59	4.9	558	2	B83583	probable acyl-CoA
998	59.5	4.9	1171	2	A42916	metabotropic gluta	1071	59	4.9	598	2	T34901	probable gamma-glu
999	59.5	4.9	1184	2	H66190	hypothetical prote	1072	59	4.9	603	2	T39688	limbirtin - fibron
1000	59.5	4.9	1262	2	T30524	protein phosphatas	1073	59	4.9	614	2	G97244	probable phosphogl
1001	59.5	4.9	1463	2	T30193	nuclear receptor c	1074	59	4.9	627	2	G97244	flagellar hook-ass
1002	59.5	4.9	1496	2	AH0447	insecticidal toxin	1075	59	4.9	639	1	E70122	1,4-alpha-glucan b
1003	59.5	4.9	1541	2	AC2474	heterocyst glycoli	1076	59	4.9	656	2	H82862	conjugal transfer
1004	59.5	4.9	1765	2	A31494	DNA-directed RNA p	1077	59	4.9	678	2	S28648	glutamate-cysteine
1005	59.5	4.9	1766	2	B31875	DNA-directed RNA p	1078	59	4.9	679	2	S28366	recombination repa
1006	59.5	4.9	1766	2	A31875	DNA-directed RNA p	1079	59	4.9	681	2	T78558	hypothetical Brach
1007	59.5	4.9	1791	2	T02345	hypothetical prote	1080	59	4.9	699	2	A38368	chitinase (EC 3.2.
1008	59.5	4.9	1876	2	C70749	probable ppsa prot	1081	59	4.9	732	2	F84394	helicase [imported
1009	59.5	4.9	2232	1	A36028	DNA-directed DNA p	1082	59	4.9	745	2	T38299	probable beta-adap
1010	59.5	4.9	2531	2	T16743	hypothetical prote	1083	59	4.9	767	2	A49546	DNA topoisomerase
1011	59.5	4.9	2617	2	AE2136	peptide synthetase	1084	59	4.9	820	2	G62168	trimethylamine-N-o
1012	59.5	4.9	3005	1	GNVSTV	genome polyprotein	1085	59	4.9	829	2	S72366	DNA topoisomerase
1013	59.5	4.9	3391	1	GNWV16	ORF 3' of ctsA - B	1086	59	4.9	888	2	D84650	probable potassium
1014	59.5	4.9	108	2	B43936	RNA polymerase ECF	1087	59	4.9	914	2	T00757	probable ubiquitin
1015	59	4.9	177	2	D83727	thioredoxin m prec	1088	59	4.9	966	1	PHPOAG	search phosphoxyla
1016	59	4.9	181	1	TXSPM	unknown protein F5	1089	59	4.9	993	2	T09129	probable erythrocy
1017	59	4.9	195	2	A96731	hypothetical prote	1090	59	4.9	1011	2	A12046	ABC transporter At
1018	59	4.9	202	2	T36368	RPE15 protein - al	1091	59	4.9	1060	2	S63252	hypothetical prote
1019	59	4.9	219	2	T03671	riboflavin-specific	1092	59	4.9	1074	2	T52654	Ca2+-transporting
1020	59	4.9	227	2	AH2318	tetrahydromethanop	1093	59	4.9	1096	2	A96607	protein disease re
1021	59	4.9	238	2	S18369	hypothetical prote	1094	59	4.9	1103	2	T42022	probable chitin sy
1022	59	4.9	241	2	G70578	hypothetical prote	1095	59	4.9	1175	2	S39951	chitin synthase (E
1023	59	4.9	242	2	T40523	hypothetical prote	1096	59	4.9	1206	2	AG2140	hypothetical prote
1024	59	4.9	244	2	AE2753	transcription regu	1097	59	4.9	1214	2	UC2069	zinc-finger protei
1025	59	4.9	252	2	D97534	probable transcript	1098	59	4.9	1234	2	S72640	endo-1,4-beta-xyla
1026	59	4.9	259	2	A27259	hypothetical rolb	1099	59	4.9	1288	2	T09908	hypothetical prote
1027	59	4.9	268	2	T10304	inhibitor of apopt	1100	59	4.9	1290	2	S73653	DNA-directed RNA p
1028	59	4.9	268	2	A53989	apoptosis-inhibiti	1101	59	4.9	1345	2	S46817	hypothetical prote
1029	59	4.9	277	1	RDHUCB	catbonyl reductase	1102	59	4.9	1541	2	S46866	hypothetical prote
1030	59	4.9	280	2	H95901	conserved hypotet	1103	59	4.9	1664	2	T18262	S-layer protein -
1031	59	4.9	285	2	A86755	prophage p12 prote	1104	59	4.9	1904	2	T13256	tail-host specific
1032	59	4.9	294	2	AD1649	weakly phage relat	1105	59	4.9	1992	1	S02771	myosin heavy chain
1033	59	4.9	296	2	AG3388	exodeoxyribonuclea	1106	59	4.9	2163	2	T15276	hypothetical prote
1034	59	4.9	297	2	B83621	probable transcript	1107	59	4.9	3175	1	RWMVY	genome polyprotein
1035	59	4.9	304	2	A89882	hypothetical prote	1108	59	4.9	9376	2	T14593	syringomycin synh
1036	59	4.9	305	2	G84568	probable xylogluca	1109	59	4.9	76	2	G87155	conserved hypotet
1037	59	4.9	330	2	A30517	lymphocyte-specifi	1110	59	4.9	126	2	G83571	heat shock hypotet
1038	59	4.9	334	2	AC0517	fructose repressor	1111	59	4.9	154	2	US0710	heat shock protein
1039	59	4.9	334	2	S15941	PEP-fructosephosph	1112	59	4.9	158	2	S16247	heat shock protein
1040	59	4.9	335	2	AD1686	peptidase homolog	1113	59	4.9	166	2	A81853	chaperone protein
1041	59	4.9	348	2	C83571	probable binding p	1114	59	4.9	173	2	T29033	hypothetical prote
1042	59	4.9	362	2	C82070	conserved hypotet	1115	59	4.9	201	2	T47123	hypothetical prote
1043	59	4.9	373	1	S04039	alcohol dehydrogen	1116	59	4.9	217	2	E70941	hypothetical prote
1044	59	4.9	378	1	T03758	probable ferredoxi	1117	59	4.9	202	2	B86476	protein F1504_41 [
1045	59	4.9	394	2	S77272	hypothetical prote	1118	59	4.9	215	2	AS1JG5	vif protein - huma
1046	59	4.9	397	2	T46717	proteinase inhibiti	1119	59	4.9	216	2	AC0715	conserved hypotet
1047	59	4.9	400	2	B97020	argininosuccinate	1120	59	4.9	234	2	B43546	T-cell receptor ga
1048	59	4.9	441	2	AG2237	hypothetical prote	1121	59	4.9	243	2	A25037	atf8B regulatory pr
1049	59	4.9	455	2	A11995	amino acid transpo	1122	59	4.9	244	2	A67633	hydrolyase, alpha/b
1050	59	4.9	460	2	A31897	muscarinic acetylch	1123	59	4.9	257	2	C87550	polysaccharide dea
1051	59	4.9	474	1	A40570	lipoprotein lipase	1124	59	4.9	258	2	AC0057	conserved hypotet

1125	58.5	4.9	258	2	T48687	hypothetical prote
1126	58.5	4.9	269	2	G63865	hypothetical prote
1127	58.5	4.9	273	2	S76948	probable creatinin
1128	58.5	4.9	277	2	I39872	conserved hypotnet
1129	58.5	4.9	280	2	B87305	metallo-beta-lacta
1130	58.5	4.9	283	2	H83860	patcohenate synth
1131	58.5	4.9	292	2	A95163	hypothetical prote
1132	58.5	4.9	292	2	H98028	hypothetical prote
1133	58.5	4.9	301	2	C75593	probable ABC trans
1134	58.5	4.9	302	2	B36866	probable transamin
1135	58.5	4.9	307	2	A96220	hypothetical prote
1136	58.5	4.9	307	2	AH3066	conserved hypotnet
1137	58.5	4.9	312	1	S73934	MG85 homolog G07_
1138	58.5	4.9	314	1	S09575	osteopontin precur
1139	58.5	4.9	317	2	G71119	probable ornithine
1140	58.5	4.9	320	2	G96714	hypothetical prote
1141	58.5	4.9	329	1	JGRCGA	L-arabinose-bindin
1142	58.5	4.9	329	1	F85803	L-arabinose-bindin
1143	58.5	4.9	329	2	A99955	L-arabinose-bindin
1144	58.5	4.9	337	2	T34964	probable regulator
1145	58.5	4.9	340	2	SI8650	homeotic protein H
1146	58.5	4.9	367	2	G71076	probable hydrogena
1147	58.5	4.9	371	2	C67446	queuine tRNA ribos
1148	58.5	4.9	381	2	G83518	probable acyl-CoA
1149	58.5	4.9	384	2	S73122	cardamoyl phosphat
1150	58.5	4.9	388	2	AC0138	ToIA collagen impor
1151	58.5	4.9	394	2	S76353	probable aspartate
1152	58.5	4.9	402	2	S75082	patcohenate metab
1153	58.5	4.9	403	2	H69362	sucinyl-diaminopi
1154	58.5	4.9	406	2	T50894	hydroxyneutropren
1155	58.5	4.9	409	2	D75629	probable transposa
1156	58.5	4.9	410	2	A59279	beta-arrestin 2 -
1157	58.5	4.9	414	2	H90815	probable kinase [i
1158	58.5	4.9	414	2	D85675	probable kinase yc
1159	58.5	4.9	414	2	C64866	probable permease
1160	58.5	4.9	421	2	C62253	folylpolyglutamate
1161	58.5	4.9	422	2	A10145	probable substrate
1162	58.5	4.9	425	2	A84849	probable RING zinc
1163	58.5	4.9	439	2	A35744	clusterin precursor
1164	58.5	4.9	443	2	T05132	hypothetical prote
1165	58.5	4.9	446	2	G70634	probable lipid prot
1166	58.5	4.9	450	2	A11671	signal recognition
1167	58.5	4.9	464	1	S37616	transcription fact
1168	58.5	4.9	465	2	AE0931	two-component syst
1169	58.5	4.9	471	2	S42631	microsome-associat
1170	58.5	4.9	472	2	G01872	selenium-binding p
1171	58.5	4.9	474	2	B64434	anthranilate synth
1172	58.5	4.9	477	1	KCHU51	stromelysin 1 (EC
1173	58.5	4.9	486	2	T18903	hypothetical prote
1174	58.5	4.9	489	2	T41446	conserved hypotnet
1175	58.5	4.9	495	2	AH0517	UDP-N-acetylmuramo
1176	58.5	4.9	505	2	H95390	probable reverse t
1177	58.5	4.9	506	2	B87102	conserved membrane
1178	58.5	4.9	506	2	F83545	hypothetical prote
1179	58.5	4.9	511	1	A32966	Cytochrome P450 4A
1180	58.5	4.9	511	1	J01935	endo-1,4-beta-xyla
1181	58.5	4.9	548	2	T04058	hypothetical prote
1182	58.5	4.9	548	2	T04058	hypothetical prote
1183	58.5	4.9	562	2	S75651	protoporphyrinogen
1184	58.5	4.9	570	2	F71049	hypothetical prote
1185	58.5	4.9	575	2	C34106	glutamine-tRNA lig
1186	58.5	4.9	579	2	T15135	protein kinase (EC
1187	58.5	4.9	609	2	S28283	hypothetical prote
1188	58.5	4.9	613	2	A81964	hypothetical prote
1189	58.5	4.9	614	2	D34106	cell division prot
1190	58.5	4.9	619	2	E84800	protein kinase (EC
1191	58.5	4.9	619	2	G84489	hypothetical prote
1192	58.5	4.9	626	2	D90069	probable TNF2-like
1193	58.5	4.9	626	2	F85295	sulfite reductase
1194	58.5	4.9	627	2	T05789	hypothetical prote
1195	58.5	4.9	657	2	S73946	hypothetical prote
1196	58.5	4.9	672	2	B82015	exonuclease ABC c
1197	58.5	4.9	678	2	B83154	probable integral
						conserved hypotnet
1198	58.5	4.9	680	2	T25832	hypothetical prote
1199	58.5	4.9	689	2	T35882	hypothetical prote
1200	58.5	4.9	690	2	T41950	glycoprotein H - h
1201	58.5	4.9	706	2	S50616	hypothetical prote
1202	58.5	4.9	714	2	T16126	hypothetical prote
1203	58.5	4.9	721	2	S29795	hypothetical prote
1204	58.5	4.9	721	2	T09631	probable acylamino
1205	58.5	4.9	728	2	B71009	hypothetical prote
1206	58.5	4.9	746	2	T29584	hypothetical prote
1207	58.5	4.9	776	2	A48480	outer capsid prote
1208	58.5	4.9	802	2	T32448	hypothetical prote
1209	58.5	4.9	822	2	AE2404	DNA helicase [lipo
1210	58.5	4.9	848	2	S48273	probable transcrip
1211	58.5	4.9	898	2	D95122	phosphoenolpyruvat
1212	58.5	4.9	931	2	D86222	protein F7G19.9 [i
1213	58.5	4.9	983	2	AG2381	glycine cleavage s
1214	58.5	4.9	984	2	T50309	hypothetical WD-re
1215	58.5	4.9	993	2	J00488	atSR protein - Str
1216	58.5	4.9	1007	2	G96606	disease resistance
1217	58.5	4.9	1040	1	T46931	alpha-mannosidase
1218	58.5	4.9	1054	1	A69975	NADPH-ferrioxopro
1219	58.5	4.9	1058	2	B95148	carbamoyl-phosphat
1220	58.5	4.9	1058	2	H98015	carbamoyl-phosphat
1221	58.5	4.9	1091	2	E71322	isoleucine-tRNA 11
1222	58.5	4.9	1092	2	S42798	fibronectin-Bindin
1223	58.5	4.9	1097	2	T31504	hypothetical prote
1224	58.5	4.9	1165	2	A48667	peroxisomal assemb
1225	58.5	4.9	1168	1	MMAX1C	myosin heavy chain
1226	58.5	4.9	1266	2	T27024	hypothetical prote
1227	58.5	4.9	1338	2	T40993	protein kinase cck
1228	58.5	4.9	1402	2	H86560	protein export [im
1229	58.5	4.9	1402	2	E72062	hypothetical prote
1230	58.5	4.9	1405	2	T27969	hypothetical prote
1231	58.5	4.9	1421	2	T49500	hypothetical prote
1232	58.5	4.9	1477	2	T00957	myosin heavy chain
1233	58.5	4.9	1626	2	A75613	hypothetical prote
1234	58.5	4.9	1704	2	T43141	vitellogenin 1 - m
1235	58.5	4.9	1768	2	T27023	hypothetical prote
1236	58.5	4.9	2109	2	T38414	transcription fact
1237	58.5	4.9	2150	1	S27802	zinc finger protei
1238	58.5	4.9	2150	2	T19450	hypothetical prote
1239	58.5	4.9	2342	2	T18200	fatty-acid synthas
1240	58.5	4.9	2588	2	A12136	peptide synthetase
1241	58.5	4.9	3512	2	T17121	cpv protein - mdg
1242	58	4.8	115	2	B97764	hypothetical prote
1243	58	4.8	137	2	AC2864	lactoylglutathione
1244	58	4.8	148	2	AC0254	conserved hypotnet
1245	58	4.8	153	2	F97641	probable lactoylgl
1246	58	4.8	158	2	H83350	hypothetical prote
1247	58	4.8	166	2	S22631	petp protein - Rho
1248	58	4.8	169	2	D65126	probable general s
1249	58	4.8	171	2	T51674	myb-related transc
1250	58	4.8	175	2	C70326	hypothetical prote
1251	58	4.8	177	2	T09495	chlorodoxin m - ra
1252	58	4.8	190	2	B95210	hypothetical prote
1253	58	4.8	190	2	E98074	hypothetical prote
1254	58	4.8	191	1	RGBY36	cell division cont
1255	58	4.8	210	2	AC2468	transcription anti
1256	58	4.8	213	2	AH2253	hypothetical prote
1257	58	4.8	218	2	H70770	probable regulator
1258	58	4.8	220	2	G85872	probable lipoprote
1259	58	4.8	224	2	B91111	hypothetical prote
1260	58	4.8	224	2	B85956	hypothetical prote
1261	58	4.8	238	2	D69021	tetrahydromethanop
1262	58	4.8	246	2	S46504	2-deoxyglucose-6-p
1263	58	4.8	250	2	AF2881	lipase esterase [i
1264	58	4.8	250	2	F97657	lipase esterase (A
1265	58	4.8	250	2	T05996	hypothetical prote
1266	58	4.8	258	2	T13263	hypothetical prote
1267	58	4.8	259	2	AE2435	hypothetical prote
1268	58	4.8	264	2	S74721	tryptophan synthas
1269	58	4.8	266	2	A12283	hypothetical prote
1270	58	4.8	275	2	A82578	glycerol uptake fa

1271	58	4.8	296	2	F72745	hypothetical prote	1344	58	4.8	663	1	A38283	arachidonate 12-11
1272	58	4.8	300	2	B65021	hypothetical prote	1345	58	4.8	664	2	S44756	hypothetical protein d
1273	58	4.8	302	2	T36030	probable fructokin	1346	58	4.8	679	2	T00636	hypothetical prote
1274	58	4.8	303	2	AH0980	glycine-cRNA ligas	1347	58	4.8	686	2	A38235	microtubule-associ
1275	58	4.8	306	2	AC2419	ornithine carbamoy	1348	58	4.8	695	2	T40451	n-terminal acetyl
1276	58	4.8	311	2	T02009	hypothetical prote	1349	58	4.8	698	1	TVFVLV	protein-lysine k
1277	58	4.8	312	2	C64511	hypothetical prote	1350	58	4.8	698	2	C96001	probable glycosyl
1278	58	4.8	322	2	A57516	DNA supercoiling f	1351	58	4.8	704	2	S46000	probable membrane
1279	58	4.8	330	2	G95187	conserved domain p	1352	58	4.8	724	2	C83706	lactibiotic metrac
1280	58	4.8	333	2	AD3284	proline racemase (1353	58	4.8	757	2	AF1755	bacteriophage prot
1281	58	4.8	337	2	AE2228	dolichol-phosphate	1354	58	4.8	767	2	JU0144	DNA topoisomerase
1282	58	4.8	337	2	S55932	NCA3 protein precu	1355	58	4.8	771	2	A10016	ferrous iron trans
1283	58	4.8	339	2	B83496	hypothetical prote	1356	58	4.8	776	1	A45395	outer layer protei
1284	58	4.8	342	2	AC2153	hypothetical prote	1357	58	4.8	793	2	A11380	exoribonuclease RN
1285	58	4.8	342	2	S42885	beta-1,3-glucanase	1358	58	4.8	796	2	T23238	hypothetical prote
1286	58	4.8	344	2	E75629	probable integrase	1359	58	4.8	798	2	T00131	xylin 1,4-beta-xy
1287	58	4.8	358	2	C72626	hypothetical prote	1360	58	4.8	800	2	T23247	hypothetical prote
1288	58	4.8	367	2	H96764	protein RING zinc	1361	58	4.8	838	1	EEWTHM	glutinin, high mol
1289	58	4.8	370	2	A46579	estrogen receptor-	1362	58	4.8	867	1	JQ1525	nitrate reductase
1290	58	4.8	375	2	T02215	ferredoxin-NADP re	1363	58	4.8	880	2	F85381	potassium channel-
1291	58	4.8	376	1	B65183	probable hydro-1ya	1364	58	4.8	898	2	JH0440	Rad54 protein - ye
1292	58	4.8	376	2	D91219	probable regulator	1365	58	4.8	916	2	T05360	probable potassium
1293	58	4.8	376	2	F86065	probable regulator	1366	58	4.8	923	2	A53054	lipoygenase (EC 1
1294	58	4.8	377	2	C86111	beta-lactamase, pe	1367	58	4.8	948	2	E82206	DnaK-related prote
1295	58	4.8	377	2	C91270	beta-lactamase (im	1368	58	4.8	952	2	T44754	probable glycine d
1296	58	4.8	379	2	C86873	transcription regu	1369	58	4.8	964	2	T41547	hypothetical prote
1297	58	4.8	388	2	A82903	conserved hypochet	1370	58	4.8	973	2	T50449	DNA repair and rec
1298	58	4.8	392	2	A49208	nitrite reductase	1371	58	4.8	1039	2	I38401	ATP-driven ion pum
1299	58	4.8	398	2	JQ0366	phospholipase C (E	1372	58	4.8	1043	2	D84900	hypothetical prote
1300	58	4.8	399	2	A53856	aryl-acylamidase (1373	58	4.8	1051	2	A40021	integrin alpha-3 c
1301	58	4.8	406	2	T03557	Rep protein - Cios	1374	58	4.8	1065	2	A43421	SEC8 protein - Yea
1302	58	4.8	407	2	G84309	hypothetical prote	1375	58	4.8	1073	2	T51055	recombination acti
1303	58	4.8	407	2	T33427	hypothetical prote	1376	58	4.8	1095	2	T01916	hypothetical prote
1304	58	4.8	420	2	T08691	hypothetical prote	1377	58	4.8	1097	2	A56138	transcription fact
1305	58	4.8	425	2	T12741	hypothetical prote	1378	58	4.8	1132	2	C75259	probable iron-sulf
1306	58	4.8	435	2	T15737	hypothetical prote	1379	58	4.8	1174	2	T08196	hypothetical prote
1307	58	4.8	437	2	H90265	heterodisulfite re	1380	58	4.8	1213	2	E69255	hemosyltransferas
1308	58	4.8	438	2	S19347	TyA protein - yeas	1381	58	4.8	1240	2	S21086	anion exchange pro
1309	58	4.8	438	2	S61589	TyA protein - yeas	1382	58	4.8	1329	2	D87226	conserved hypochet
1310	58	4.8	440	2	C84553	probable protein k	1383	58	4.8	1522	2	T39371	transcription regu
1311	58	4.8	443	2	T17220	hypothetical prote	1384	58	4.8	1770	2	S69948	TyB protein - yeas
1312	58	4.8	469	2	B95958	probable glucuron	1385	58	4.8	1810	2	S53592	TyB protein - yeas
1313	58	4.8	478	2	S69974	TyA protein - yeas	1386	58	4.8	1810	2	S69973	TyB protein - yeas
1314	58	4.8	484	2	T17756	probable chitinase	1387	58	4.8	2958	2	S64921	probable membrane
1315	58	4.8	497	2	JB0275	voltage-gated pota	1388	58	4.8	3534	2	T42367	tegment protein 2
1316	58	4.8	499	2	AC2128	ferrichrome-iron r	1389	58	4.8	4861	2	S71752	giant protein p619
1317	58	4.8	504	2	T38226	probable serine-th	1390	57.5	4.8	72	2	AB3232	entry-exclusion pr
1318	58	4.8	516	2	A86148	hypothetical prote	1391	57.5	4.8	114	2	S72940	hypothetical prote
1319	58	4.8	517	2	JC7623	protein disulfide-	1392	57.5	4.8	132	2	B82403	hypothetical prote
1320	58	4.8	519	2	S74242	6-phosphofructo-2-	1393	57.5	4.8	144	2	T50076	probable 50S ribos
1321	58	4.8	527	2	S39549	thioglycosidase (E	1394	57.5	4.8	151	2	S21600	heat shock protein
1322	58	4.8	529	2	T50609	hypothetical prote	1395	57.5	4.8	154	2	S12629	heat shock cognate
1323	58	4.8	530	2	B84130	two-component resp	1396	57.5	4.8	158	2	B64864	ycsN protein - Bac
1324	58	4.8	541	2	B95220	dextran glucosidas	1397	57.5	4.8	158	2	D90838	hypothetical prote
1325	58	4.8	541	2	H98083	dextranase (BC 3.2	1398	57.5	4.8	158	2	D85696	hypothetical prote
1326	58	4.8	550	2	AB0166	probable prismane	1399	57.5	4.8	162	2	B87655	conserved hypochet
1327	58	4.8	550	2	H84476	probable AtnA1a re	1400	57.5	4.8	176	2	B75015	ddp-4-keto-1-tham
1328	58	4.8	555	1	HNNZSV	hemagglutinin-neur	1401	57.5	4.8	202	2	H86566	phosphatase/kinase
1329	58	4.8	576	2	T17842	hypothetical prote	1402	57.5	4.8	206	2	A84865	probable glutathio
1330	58	4.8	578	2	B90578	lipoprotein a (lmp	1403	57.5	4.8	209	2	S30541	prolactin precursor
1331	58	4.8	586	2	A41125	gamma-glutamyltran	1404	57.5	4.8	216	2	T38897	hypothetical prote
1332	58	4.8	595	2	B72801	gpi3 protein - Myc	1405	57.5	4.8	228	2	C70164	rRNA methylase (ya
1333	58	4.8	604	2	T20875	hypothetical prote	1406	57.5	4.8	229	2	D83250	cytidylate kinase
1334	58	4.8	612	1	W1WLE	El protein - human	1407	57.5	4.8	237	2	C75035	arginase related p
1335	58	4.8	631	2	G64874	probable membrane	1408	57.5	4.8	241	2	E75064	hypothetical prote
1336	58	4.8	640	2	G72339	threonine-cRNA lig	1409	57.5	4.8	243	2	T38519	protein T12C24.18
1337	58	4.8	645	2	T39614	conserved hypobet	1410	57.5	4.8	246	2	B86260	hypothetical prote
1338	58	4.8	645	2	A75533	negative regulator	1411	57.5	4.8	251	2	S23889	hypothetical prote
1339	58	4.8	646	2	T48644	2',3'-cyclic-nucle	1412	57.5	4.8	252	2	AH2105	hypothetical prote
1340	58	4.8	647	1	ESSEPC	2',3'-cyclic-nucle	1413	57.5	4.8	253	2	A32187	triose-phosphate 1
1341	58	4.8	647	1	G86118	2',3'-cyclic-nucle	1414	57.5	4.8	255	2	B87595	transcription regu
1342	58	4.8	647	1	G91277	DNA-directed RNA p	1415	57.5	4.8	264	1	E70027	probable 3-oxoacyl
1343	58	4.8	649	2	H90163		1416	57.5	4.8	265	2	AG0814	cob(I)alamin adeno

1417	57.5	4.8	267	1	CTPBP	corticotropin / 11
1418	57.5	4.8	268	2	ATG137	hypothetical prote
1419	57.5	4.8	275	2	F81675	conserved hypothec
1420	57.5	4.8	277	2	T21922	hypothetical prote
1421	57.5	4.8	280	2	E82642	phage-related prot
1422	57.5	4.8	281	2	S39495	u-plasmenogen acti
1423	57.5	4.8	282	2	AP3033	aldolase Adu875
1424	57.5	4.8	287	2	P98252	probable aldolase
1425	57.5	4.8	292	2	I77525	probable aldolase
1426	57.5	4.8	294	2	P98061	glucokinase [ampom
1427	57.5	4.8	294	2	AS9195	ROK family protein
1428	57.5	4.8	296	2	I46021	Pc-gamma receptor
1429	57.5	4.8	296	2	G02066	biliverdin reducta
1430	57.5	4.8	298	2	D63351	hypothetical prote
1431	57.5	4.8	299	2	F85835	hypothetical prote
1432	57.5	4.8	299	2	D90990	hypothetical prote
1433	57.5	4.8	300	2	S27780	major merozoite su
1434	57.5	4.8	303	2	I77524	prolactin receptor
1435	57.5	4.8	304	2	T42521	probable urp-gluc
1436	57.5	4.8	305	2	AD5157	transcription regu
1437	57.5	4.8	307	1	RWMSBC	T-cell receptor be
1438	57.5	4.8	308	2	G71454	hypothetical prote
1439	57.5	4.8	309	2	S28595	glycophorin-bindin
1440	57.5	4.8	312	2	T45739	transcription fact
1441	57.5	4.8	312	2	G84305	hypothetical prote
1442	57.5	4.8	319	2	AF0228	probable transpos
1443	57.5	4.8	319	2	S49771	hypothetical prote
1444	57.5	4.8	320	2	H64332	hypothetical prote
1445	57.5	4.8	320	2	D98130	hypothetical prote
1446	57.5	4.8	333	2	S46984	probable transcrip
1447	57.5	4.8	333	2	AS3743	indole-3-pyruvate
1448	57.5	4.8	338	2	AH3463	u-plasmenogen acti
1449	57.5	4.8	338	2	DT0308	hypothetical prote
1450	57.5	4.8	340	2	AD4008	conserved hypothet
1451	57.5	4.8	341	2	S45865	homeotic protein H
1452	57.5	4.8	349	2	C95866	P26f3.4 protein (d
1453	57.5	4.8	353	2	AB3456	probable fructose-
1454	57.5	4.8	354	2	I80165	arginine/ornithine
1455	57.5	4.8	360	2	C64628	class I diacylcompa
1456	57.5	4.8	363	2	T06620	lipid A disacchari
1457	57.5	4.8	370	2	AA1891	hypothetical prote
1458	57.5	4.8	377	2	H71081	basal body P-ring
1459	57.5	4.8	386	2	T26108	hypothetical prote
1460	57.5	4.8	387	2	G87537	acyl-CoA dehydrog
1461	57.5	4.8	389	2	H90413	hypothetical prote
1462	57.5	4.8	391	2	AG3243	conserved hypothec
1463	57.5	4.8	399	2	B85675	conjugal transfer
1464	57.5	4.8	399	2	AE4856	lipoprotein releasa
1465	57.5	4.8	399	2	P90815	lipoprotein releasa
1466	57.5	4.8	407	2	H69064	serine/threonine p
1467	57.5	4.8	410	2	I39766	glutamate N-acetyl
1468	57.5	4.8	410	2	S15163	probable transpos
1469	57.5	4.8	414	2	E90572	hypothetical prote
1470	57.5	4.8	414	2	AD2193	hypothetical prote
1471	57.5	4.8	417	2	DS5614	transcription regu
1472	57.5	4.8	417	2	D91297	probable nadab tra
1473	57.5	4.8	417	2	F86138	probable nadab tra
1474	57.5	4.8	421	2	T03421	trab protein - Agr
1475	57.5	4.8	423	1	VHNVSB	structural polyprot
1476	57.5	4.8	434	2	C95163	NOL1/NO22/gun fam
1477	57.5	4.8	435	2	S27453	meiotic recombinat
1478	57.5	4.8	445	2	AG3591	DNA polymerase IV
1479	57.5	4.8	450	2	AA4751	carotenoid-binding
1480	57.5	4.8	452	2	AE6174	rRNA nucleotidyltr
1481	57.5	4.8	456	2	T46478	serine/threonine p
1482	57.5	4.8	457	2	S08162	nicotinic acetylch
1483	57.5	4.8	462	2	AA1158	dipeptidyl-peptida
1484	57.5	4.8	462	2	AH0302	phosphomannomuta
1485	57.5	4.8	467	1	J02315	major capsid prote
1486	57.5	4.8	472	2	AB6347	branched-chain alp
1487	57.5	4.8	472	2	TS1858	branched-chain alp
1488	57.5	4.8	492	2	S65238	probable membrane
1489	57.5	4.8	494	2	A96793	probable DNA-bind

1490	57.5	4.8	499	2	T16168	uridylyltransferase
1491	57.5	4.8	500	2	A51963	hypothetical prote
1492	57.5	4.8	503	2	B82699	carboxypeptidase r
1493	57.5	4.8	506	2	T40935	probable utp-glucose
1494	57.5	4.8	507	2	E71551	probable monooxygen
1495	57.5	4.8	508	2	C72074	hypothetical prote
1496	57.5	4.8	518	2	N18048	nitrogenase (BC 1.
1497	57.5	4.8	519	1	B90548	conserved hypothet
1498	57.5	4.8	528	2	B75364	extracellular solut
1499	57.5	4.8	528	2	E71525	probable ABC trans
1500	57.5	4.8	530	2	E712125	ABC transporter pr

ALIGNMENTS

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Title: US-10-036-214-61

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Sequence: 1 MGWTRLVATLALGLMMVV.....PTIQAPRGASPEPKTKRQR 223

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1196	99.3	223	1	PBPL_HUMAN
2	561.5	49.6	242	1	PEBP_MOUSE
3	385.5	32.0	202	2	O66KX5
4	260.5	21.6	211	2	O66PT6
5	258.5	21.5	224	2	O7QHW0
6	246	20.4	214	2	O7PYW1
7	236	19.6	191	2	O7PYW6
8	235.5	19.5	186	1	PEBP_RAT
9	234.5	19.5	221	1	PEBP_CAEEL
10	231	19.2	152	1	D1_ONCVO
11	231	19.2	179	2	O670U4
12	229	19.0	257	2	O9VK60
13	225	18.7	186	1	PEBP_MOUSE
14	223	18.5	134	1	D3_ONCVO
15	222.5	18.5	187	2	O9V108
16	222	18.4	197	1	OYV16_ONCVO
17	219	18.2	114	1	D2_ONCVO
18	218.5	18.1	186	1	PEBP_BOVIN
19	218.5	18.1	187	1	PEBP_MOUSE
20	216.5	18.0	202	2	O9V109
21	213.5	17.7	187	2	O6VYS4
22	211.5	17.6	187	2	O6MK67
23	210.5	17.5	187	2	O7ZUV8
24	206	17.1	186	1	PEBP_MACPA
25	205	17.0	173	1	MFT_ARATH
26	205	17.0	186	1	PEBP_HUMAN
27	204.5	17.0	176	2	O656T5
28	203	16.9	121	2	O9D9L5
29	202	16.8	186	2	O6GPR7
30	199	16.5	135	2	O87AK8
31	199	16.5	186	2	O6IRMO

32	197.5	16.4	241	2	O7PYP5	O7PYP5 anopheles g
33	196	16.3	111	2	O9NRY4	O9NRY4 dirofilaria
34	195	16.2	178	2	O84XL1	O84XL1 lycopersico
35	194.5	16.2	241	2	O7OHV9	O7OHV9 anopheles g
36	192.5	16.0	173	2	O6LSN9	O6LSN9 populus nig
37	187.5	15.6	177	2	O84XL0	O84XL0 lycopersico
38	186.5	15.5	179	2	O9VD02	O9VD02 dirosophila
39	186	15.4	174	2	O76E05	O76E05 populus nig
40	185	15.4	174	2	O76CC3	O76CC3 populus nig
41	185	15.4	178	2	O8VWH2	O8VWH2 oryza sativ
42	183	15.2	172	2	O9XW37	O9XW37 caenorhabdi
43	183	15.2	174	2	O6R3R0	O6R3R0 populus del
44	183	15.2	174	2	O76B33	O76B33 populus nig
45	183	15.2	177	1	BFT_ARATH	O91L4 arabidopsis
46	182	15.1	175	1	TSP_ARATH	O9875 arabidopsis
47	182	15.1	179	2	O93MT9	O93MT9 oryza sativ
48	182	15.1	179	2	O93MT7	O93MT7 oryza sativ
49	181.5	15.1	211	2	O917L3	O917L3 dirosophila
50	181	15.0	210	1	O8AS_DROME	O9185 dirosophila
51	179	14.9	177	2	O9SXY9	O9SXY9 citus unsh
52	177.5	14.7	176	2	O6XHR8	O6XHR8 dirosophila
53	177.5	14.6	174	2	O9ASJ1	O9ASJ1 oryza sativ
54	175.5	14.6	176	2	O9VD01	O9VD01 dirosophila
55	175	14.5	174	2	O76CA4	O76CA4 populus nig
56	173	14.4	185	2	O6EUP9	O6EUP9 oryza sativ
57	172	14.3	174	2	O76B44	O76B44 populus nig
58	169.5	14.1	262	1	TB26_TOXCA	P54190 toxocara ca
59	168.5	14.0	175	2	O84XK9	O84XK9 lycopersico
60	168	14.0	151	2	O70JR7	O70JR7 triticum ae
61	168	14.0	173	2	O75QW9	O75QW9 populus nig
62	166.5	13.8	173	2	O75QX2	O75QX2 populus nig
63	166	13.8	174	2	O75QW8	O75QW8 malus domes
64	165.5	13.7	173	2	O7XAB3	O7XAB3 pisum sativ
65	164.5	13.7	176	2	O9FTP7	O9FTP7 oryza sativ
66	164	13.6	174	1	CET1_TOBAC	O9Xh4 nicotiana t
67	164	13.6	175	1	FT_ARATH	O9Xx2 arabidopsis
68	162.5	13.5	194	2	O6CFV4	O6CFV4 yarrowia li
69	162	13.5	229	2	O70A07	O7Qa7 anopheles g
70	160.5	13.3	172	2	O84XK7	O84XK7 lycopersico
71	160	13.3	174	2	O7XUP1	O7XUP1 oryza sativ
72	159	13.2	182	2	O9Y1K8	O9Y1K8 octopus dof
73	155.5	12.9	212	2	O6B8B9	O6B8B9 debaryomyce
74	154.5	12.8	173	2	O9XGS4	O9XGS4 oryza sativ
75	154	12.8	145	2	O70JR8	O70JR8 triticum ae
76	153.5	12.7	174	2	O6VGS8	O6VGS8 pisum sativ
77	152	12.6	173	2	O9XGS5	O9XGS5 oryza sativ
78	152	12.6	174	2	O6LSU7	O6LSU7 populus nig
79	152	12.6	174	2	O6TXM3	O6TXM3 populus tri
80	152	12.6	174	2	O76FW2	O76FW2 populus nig
81	150	12.5	172	2	O76M79	O76M79 malus domes
82	150	12.5	175	2	O6BS90	O6BS90 debaryomyce
83	148.5	12.3	175	1	SP_LYCES	O82088 lycopersico
84	148	12.3	181	1	CEN_ANTPA	O41261 antirrhinum
85	147.5	12.3	175	1	CET2_TOBAC	O9Xh3 nicotiana t
86	147	12.2	175	1	CEN_ARATH	O9ZNV5 arabidopsis
87	146.5	12.2	173	2	O69FJ7	O69FJ7 citus sine
88	145	12.0	204	2	O751Y1	O751Y1 ashbya goss
89	144.5	12.0	175	1	CET4_TOBAC	O9Xh4 nicotiana t
90	143.5	11.9	105	2	O96K00	O96K00 homo sapien
91	143	11.9	173	2	O8LML8	O8LML8 vicia vint
92	142.5	11.8	173	2	O8LSG7	O8LSG7 arabidopsis
93	141	11.7	173	2	O6LSU5	O6LSU5 populus nig
94	140	11.6	173	2	O6ESR8	O6ESR8 oryza sativ
95	139.5	11.6	140	2	O84XK8	O84XK8 lycopersico
96	138	11.5	118	2	O9XH41	O9XH41 nicotiana t
97	138	11.5	173	2	O7XVG4	O7XVG4 oryza sativ
98	137.5	11.4	177	1	TFL1_ARATH	P33003 arabidopsis
99	137.5	11.4	177	2	O8LSG9	O8LSG9 arabidopsis
100	137.5	11.4	177	2	O8LSH0	O8LSH0 arabidopsis
101	137.5	11.4	190	2	BBP_PLAFA	P54189 plasmodium
102	137.5	11.4	190	2	O7KQK1	O7KQK1 plasmodium
103	133	11.0	174	2	O6TDS5	O6TDS5 lotus japon
104	133	11.0	177	2	O9SAY4	O9SAY4 brassica ol

105	133	11.0	178	2	082152	082152 brassica na	178	91	7.6	179	2	0829C7	0829C7 streptomyc
106	133	11.0	178	2	09SA5S	09SA5S brassica na	179	91	7.6	179	2	06BRK0	06BRK0 debaryomyc
107	133	11.0	201	1	YL79_YEAST	006552 saccharomyc	180	90.5	7.5	209	2	09KJ06	09KJ06 thauera aro
108	131	10.9	178	2	082153	082153 brassica ca	181	90	7.5	179	2	074MM9	074MM9 nanocartheau
109	131	10.9	178	2	09XGD4	09XGD4 brassica ca	182	89.5	7.4	176	1	YL40_MYCTU	P67226 mycobacteri
110	130	10.9	203	2	066XH8	066XH8 dictyosteli	183	89.5	7.4	176	1	YL64_MYCBO	P67227 mycobacteri
111	130	10.8	210	2	06FX79	06FX79 candida gla	184	89.5	7.4	346	2	096DV4	096DV4 homo sapien
112	129.5	10.8	177	2	08LSG8	08LSG8 arabidopsis	185	89.5	7.4	1505	2	08IM99	08IM99 drosophila
113	129.5	10.8	197	2	06CUM6	06CUM6 kluyveromyc	186	89.5	7.4	1705	1	PPPV_MOUSE	P70289 mus musculu
114	128	10.6	197	2	09FU6A	09FU6A lolium pere	187	89.5	7.4	1945	2	0966B1	0966B1 drosophila
115	127	10.5	190	2	07RNG5	07RNG5 plasmodium	188	89.5	7.4	1945	2	09VA91	09VA91 drosophila
116	122.5	10.2	219	1	CPY1_YEAST	PI4306 saccharomyc	189	89	7.4	170	2	062FV1	062FV1 burkholderi
117	121	10.0	178	2	09SA16	09SA16 brassica na	190	89	7.4	170	2	063W40	063W40 burkholderi
118	117	9.7	168	2	07QN27	07QN27 anopheles g	191	88.5	7.4	194	2	08UDU5	08UDU5 methanobact
119	115	9.6	202	2	08ML68	08ML68 drosophila	192	88.5	7.4	426	2	08ET17	08ET17 oceanoditreil
120	114	9.5	177	2	082154	082154 brassica ol	193	88	7.3	159	2	08ELZ0	08ELZ0 shewanella
121	113.5	9.4	58	2	084LD8	084LD8 metrosidero	194	88	7.3	161	2	06ISR5	06ISR5 oryza sativ
122	113.5	9.4	181	2	06NBM7	06NBM7 rhodospseudo	195	88	7.3	174	2	09P0B9	09P0B9 homo sapien
123	113.5	9.4	201	1	YJ10_MYCTU	P67222 mycobacteri	196	88	7.3	387	2	021608	021608 caenorhabdi
124	113.5	9.4	201	1	YJ45_MYCBO	P67223 mycobacteri	197	87.5	7.3	251	2	06DB35	06DB35 erwinia car
125	113	9.4	149	2	0975D2	0975D2 sulfolobus	198	87.5	7.3	1705	2	09ERK5	09ERK5 mus musculu
126	113	9.4	151	1	Y273_METTH	026373 methanobact	199	87	7.2	150	1	Y109_CHLMU	09P140 chlamydia m
127	113	9.4	244	2	09P6X9	09P6X9 neurospora	200	86.5	7.2	150	1	Y736_CHLTR	084741 chlamydia t
128	110.5	9.2	154	2	092G37	092G37 rickettsia	201	86.5	7.2	179	2	06NH78	06NH78 corynebacte
129	109.5	9.1	58	2	084LD7	084LD7 metrosidero	202	86	7.1	153	2	06ASW8	06ASW8 propionibac
130	109.5	9.1	145	2	06L2W8	06L2W8 picropophilus	203	86	7.1	1114	2	07UZ36	07UZ36 rhodopirell
131	108.5	9.0	143	2	082XS1	082XS1 nitrosomona	204	85.5	7.1	438	2	08LS73	08LS73 chenopodium
132	108.5	9.0	181	2	072MM8	072MM8 leptospira	205	85.5	7.1	483	2	0813K8	0813K8 bacillus ce
133	108.5	9.0	181	2	08E2L4	08E2L4 leptospira	206	85.5	7.1	490	1	ACM4_CHICK	PI7200 gallus gall
134	106.5	8.8	179	2	07MCG5	07MCG5 vibrio vuln	207	85	7.1	165	2	08H0B8	08H0B8 eritricum ae
135	106.5	8.8	179	2	08DS14	08DS14 vibrio vuln	208	85	7.1	243	2	08Y271	08Y271 ralbstonia s
136	106.5	8.8	203	2	08RTQV5	08RTQV5 methanobact	209	85	7.1	757	2	06CLJ6	06CLJ6 kluyveromyc
137	106	8.8	171	1	YC50_AQUAE	067293 aquifex aeo	210	83.5	6.9	857	2	0746A8	0746A8 thermus thg
138	106	8.8	181	1	07NTA2	07NTA2 chromobacte	211	83.5	6.9	3251	2	08K4E0	08K4E0 mus musculu
139	105.5	8.8	105	2	084M17	084M17 vitis vinif	212	83	6.9	595	1	SNX9_HUMAN	G9Y5X1 homo sapien
140	105	8.7	198	1	YC69_PYRHO	058984 pyrococcus	213	83	6.9	2253	2	P70012	P70012 xenopus lae
141	104	8.6	152	2	0988D1	0988D1 rhizobium l	214	82.5	6.9	311	2	06A084	06A084 mus musculu
142	104	8.6	182	2	082063	082063 salmoneila	215	82.5	6.9	420	2	08Y315	08Y315 mycobacteri
143	103.5	8.6	58	2	07Y1X3	07Y1X3 arabidopsis	216	82	6.8	176	2	09CC45	09CC45 mycobacteri
144	103.5	8.6	177	2	09ADN9	09ADN9 streptomyc	217	82	6.8	198	2	061629	061629 oryza sativ
145	103	8.6	354	2	06C3U0	06C3U0 yarrowia li	218	82	6.8	911	2	09P2J7	09P2J7 homo sapien
146	103	8.6	416	2	09VY48	09VY48 drosophila	219	82	6.8	1072	2	070XK8	070XK8 homo sapien
147	101.5	8.4	150	2	0821P9	0821P9 chlamydomphi	220	82	6.8	1074	2	068DA5	068DA5 homo sapien
148	101.5	8.4	177	2	0871W2	0871W2 vibrio para	221	81.5	6.8	164	2	09FS18	09FS18 hordeum vul
149	100	8.3	183	2	08CXY8	08CXY8 escherichia	222	81.5	6.8	177	2	08N0J5	08N0J5 corynebacte
150	100	8.3	183	2	083KN3	083KN3 shigella fl	223	81.5	6.8	289	2	081RJ2	081RJ2 bacillus an
151	100	8.3	216	2	09HND1	09HND1 halobacteri	224	81.5	6.8	289	2	06HJ57	06HJ57 bacillus th
152	98.5	8.2	191	2	08KET2	08KET2 chlorobium	225	81.5	6.8	421	2	07TTU6	07TTU6 prochloroco
153	98	8.1	91	2	06V9P7	06V9P7 pisum sativ	226	81.5	6.8	813	2	08VUD9	08VUD9 streptococc
154	97.5	8.1	210	2	06D4D5	06d4d5 erwinia car	227	80.5	6.7	177	2	08FTC4	08FTC4 corynebacte
155	96.5	8.0	150	1	Y877_CHLPPN	092729 chlamydia p	228	80.5	6.7	186	2	055QH9	055QH9 manheimela
156	96.5	8.0	177	2	09FEB6	09FEB60 corynebacte	229	80.5	6.7	287	1	Y698_ARCFU	028575 archaeoglob
157	96.5	8.0	346	2	08K2M0	08K2M0 mus musculu	230	80.5	6.7	370	2	09L7E7	09L7E7 arabidopsis
158	96.5	8.0	346	2	0991M1	0991M1 mus musculu	231	80.5	6.7	495	2	084W11	084W11 arabidopsis
159	96.5	8.0	346	2	066GM2	066GM2 xenopus lae	232	80.5	6.7	533	2	09F121	09F121 arabidopsis
160	96	8.0	239	2	094J24	094J24 oryza sativ	233	80.5	6.7	1032	2	071Y05	071Y05 listeria mo
161	96	8.0	345	2	06NWB9	06nwb9 brachydanio	234	80	6.6	176	2	073Y60	073Y60 mycobacteri
162	95.5	7.9	290	2	08BTZ1	08BTZ1 mus musculu	235	80	6.6	178	2	06AHD8	06AHD8 leifsonia x
163	95	7.9	169	2	092T75	092T75 rhizobium m	236	80	6.6	359	2	06DBN8	06DBN8 arabidopsis
164	95	7.9	183	1	YBCL_BCOLI	P77268 escherichia	237	80	6.6	464	2	09L7O3	09L7O3 arabidopsis
165	95	7.9	191	2	06ZGF5	06ZGF5 burkholderi	238	80	6.6	520	2	068HC6	068HC6 coccidioid
166	95	7.9	198	2	063PY0	063PY0 burkholderi	239	80	6.6	577	2	06WHR2	06WHR2 deminaz
167	95	7.9	205	1	YJ11_MYCTU	P67224 mycobacteri	240	80	6.6	625	2	06GQJ3	06GQJ3 xenopus lae
168	95	7.8	205	1	YJ46_MYCBO	P67225 mycobacteri	241	80	6.6	1557	2	0874V8	0874V8 podospora a
169	94.5	7.8	417	2	07OEH4	07OEH4 anopheles g	242	79.5	6.6	300	2	06DCJ2	06DCJ2 xenopus lae
170	93.5	7.8	157	2	09UXF4	09uxf4 sulfolobus	243	79.5	6.6	328	2	095061	095061 homo sapien
171	93.5	7.8	186	1	YB53_PYRAB	09uxj3 pyrococcus	244	79.5	6.6	595	1	SNX9_MOUSE	091V42 mus musculu
172	93	7.7	180	2	09KT30	09KT30 vibrio chol	245	79.5	6.6	702	2	09AN74	09AN74 bradyrhizob
173	92.5	7.7	165	2	06SS87	06SS87 manheimela	246	79	6.6	352	2	072H38	072H38 thermus the
174	92	7.6	179	1	YH94_SPPCO	09X287 streptomyc	247	79	6.6	1004	1	YD83_SCHPO	Q10408 schizosacch
175	92	7.6	206	2	073ZG5	073ZG5 mycobacteri	248	78.5	6.5	162	2	09M042	09M042 arabidopsis
176	91.5	7.6	206	2	08XTT0	08XTT0 ralbstonia s	249	78.5	6.5	278	2	08PCJ7	08PCJ7 xanthomonas
177	91.5	7.6	551	1	SYE_ARCFU	029979 archaeoglob	250	78.5	6.5	397	1	TBXT_CHICK	P79776 gallus gall

251	78.5	6.5	417	2	Q7Q8M5	Q7Q8M5 anopheles g	324	75	6.2	257	2	Q8KGU0	Q8KGU0 rhizobium 1
252	78.5	6.5	677	2	Q8R251	Q8R251 mus musculus	325	75	6.2	267	2	Q8XV04	Q8XV04 ralestridia s
253	78.5	6.5	SYM	1	SYM_METMA	Q8Y14 mus musculus	326	75	6.2	267	2	Q8GJ44	Q8GJ44 clostridium
254	78.5	6.5	805	2	Q6CYR7	Q6CYR7 erwina car	327	75	6.2	654	2	Q8GJ44	Q8GJ44 porphyromon
255	78.5	6.5	1069	2	Q8CB37	Q8CB37 mus musculus	328	75	6.2	670	2	Q7MT53	Q7MT53 shewanella
256	78.5	6.5	1102	1	PLIG_PIG	Q02697 sus scrofa	329	75	6.2	862	2	Q22354	Q22354 caenorhabdi
257	78	6.5	278	2	Q6P029	Q6P029 brachydanio	330	75	6.2	980	1	BOB1_YEAST	P38041 saccharomyc
258	78	6.5	345	2	Q7RU21	Q7RU21 bacteriopho	331	75	6.2	1041	1	EGT2_YEAST	P48235 saccharomyc
259	78	6.5	305	2	Q76YG3	Q76YG3 neurospora	332	75	6.2	1091	2	Q6CORS	Q6CORS kluyveromyc
260	78	6.5	390	2	Q9P3C0	Q9P3C0 neurospora	333	75	6.2	1419	2	Q9V7K0	Q9V7K0 dirosophila
261	78	6.5	454	1	APR2_ARATH	P92981 a 5'-adenyl	334	75	6.2	1638	2	Q9N8E7	Q9N8E7 trypanosoma
262	78	6.5	1105	2	Q6FTE7	Q6FTE7 candida gla	335	75	6.2	3041	2	Q7SGH3	Q7SGH3 neurospora
263	78	6.5	1976	2	Q8D4R5	Q8D4R5 vibrio vuln	336	74.5	6.2	148	2	Q81EM1	Q81EM1 bacillus ce
264	77.5	6.4	158	2	Q9AP09	Q9AP09 uncultured	337	74.5	6.2	278	2	Q8PPA5	Q8PPA5 xanthomonas
265	77.5	6.4	169	2	Q7ALB6	Q7ALB6 lactobacill	338	74.5	6.2	291	2	Q7ZVD1	Q7ZVD1 brachydanio
266	77.5	6.4	170	2	Q9UVU0	Q9UVU0 pneumocysti	339	74.5	6.2	301	2	Q8C183	Q8C183 mus musculus
267	77.5	6.4	170	2	Q9CKX1	Q9CKX1 pneumocysti	340	74.5	6.2	451	2	Q6NY93	Q6NY93 brachydanio
268	77.5	6.4	185	2	Q935T5	Q935T5 streptococc	341	74.5	6.2	451	2	Q7ZM80	Q7ZM80 brachydanio
269	77.5	6.4	185	2	Q70CA5	Q70CA5 streptococc	342	74.5	6.2	454	2	Q9T2C6	Q9T2C6 caenorhabdi
270	77.5	6.4	264	2	Q7S8A3	Q7S8A3 neurospora	343	74.5	6.2	564	2	Q7Q0Q2	Q7Q0Q2 giardia lam
271	77.5	6.4	278	2	Q8C9N9	Q8C9N9 mus musculus	344	74.5	6.2	680	2	Q52644	Q52644 ruminococcu
272	77.5	6.4	306	2	Q7VVI7	Q7VVI7 bordetella	345	74.5	6.2	686	1	PL2_HUMAN	Q9NP60 h x-linked
273	77.5	6.4	328	2	Q8CXX0	Q8CXX0 mus musculu	346	74.5	6.2	689	2	Q7RYB6	Q7RYB6 neurospora
274	77.5	6.4	391	2	Q93DN3	Q93DN3 rhodococcus	347	74.5	6.2	889	2	Q7UYD6	Q7UYD6 rhodopirell
275	77.5	6.4	391	2	Q9XAU0	Q9XAU0 rhodococcus	348	74.5	6.2	1009	2	Q7P0K9	Q7P0K9 anopheles g
276	77.5	6.4	534	2	Q46778	Q46778 escherichia	349	74.5	6.2	1036	2	Q8Y5P1	Q8Y5P1 listeria mo
277	77.5	6.4	1130	1	REPT_MOUSE	P97347 mus musculu	350	74.5	6.2	1098	2	Q6NTI2	Q6NTI2 brachydanio
278	77.5	6.4	1159	2	Q7ZWM1	Q7ZWM1 brachydanio	351	74.5	6.2	1134	2	Q6PFT5	Q6PFT5 drosophila
279	77.5	6.4	1411	2	Q73Y53	Q73Y53 mycobacteri	352	74.5	6.2	1394	2	Q8MST1	Q8MST1 drosophila
280	77.5	6.4	1564	2	Q6DFB8	Q6DFB8 xenopus lae	353	74.5	6.2	1402	2	Q6FZM0	Q6FZM0 bartonella
281	77.5	6.4	2473	2	Q7Q876	Q7Q876 anopheles g	354	74.5	6.2	1511	2	Q7QAA3	Q7QAA3 anopheles g
282	77	6.4	748	2	Q87EY4	Q87EY4 xyloella fas	355	74.5	6.2	1511	2	Q9VB21	Q9VB21 drosophila
283	77	6.4	1024	2	Q642C9	Q642C9 rattus norv	356	74.5	6.2	2607	1	Q9VB21	Q9VB21 bacillus li
284	77	6.4	1622	1	DM1_RAT	Q64H33 pneumocysti	357	74	6.1	148	2	Q97BG5	Q97BG5 thermoplasma
285	77	6.4	237	2	Q8U3G8	Q8U3G8 rattus norv	358	74	6.1	159	2	Q7Q585	Q7Q585 anopheles g
286	76.5	6.4	298	2	Q9FC20	Q9FC20 streptomyc	359	74	6.1	172	2	Q6K1K7	Q6K1K7 mycoplasma
287	76.5	6.4	306	2	Q7W1L2	Q7W1L2 bordetella	360	74	6.1	190	2	Q8R2H8	Q8R2H8 oryza sativ
288	76.5	6.4	360	2	Q7V467	Q7V467 prochloroco	361	74	6.1	277	2	Q6MQ13	Q6MQ13 bdellovibri
289	76.5	6.4	376	2	Q8Z393	Q8Z393 salmoneila	362	74	6.1	292	2	Q8CSR0	Q8CSR0 staphylococ
290	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	363	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
291	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	364	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
292	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	365	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
293	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	366	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
294	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	367	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
295	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	368	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
296	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	369	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
297	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	370	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
298	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	371	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
299	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	372	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
300	76.5	6.4	434	2	Q95Y93	Q95Y93 homo sapien	373	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
301	76	6.3	130	1	APAG_RHOPA	Q7N747 photothabu	374	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
302	76	6.3	349	2	Q7N747	Q7N747 photothabu	375	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
303	76	6.3	362	2	Q8C9S4	Q8C9S4 mus musculu	376	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
304	76	6.3	410	2	Q8IAN7	Q8IAN7 bacillus ce	377	74	6.1	319	1	YD84_LISMO	Q82BX1 listeria in
305	76	6.3	463	2	Q9RNM3	Q9RNM3 xymomonas m	378	73.5	6.1	240	1	Q73YR4	Q73YR4 mus musculu
306	76	6.3	748	1	MEPA_RAT	Q64302 rattus norv	379	73.5	6.1	240	1	Q73YR4	Q73YR4 mus musculu
307	76	6.3	857	2	Q9FR78	Q9FR78 oryza sativ	380	73.5	6.1	249	2	Q93P66	Q93P66 microscilla
308	76	6.3	917	2	Q8CUC0	Q8CUC0 mus musculu	381	73.5	6.1	260	2	Q73SP3	Q73SP3 mycobacteri
309	76	6.3	1415	2	Q6PD88	Q6PD88 brachydanio	382	73.5	6.1	287	2	Q6CGB9	Q6CGB9 yarrowia li
310	76	6.3	1430	2	Q9VX86	Q9VX86 drosophila	383	73.5	6.1	316	2	Q7U8G9	Q7U8G9 synechococ
311	76	6.3	2378	2	Q6RKF4	Q6RKF4 cochljobolu	384	73.5	6.1	316	2	Q911B9	Q911B9 pseudomonas
312	75.5	6.3	218	2	Q8T4N0	Q8T4N0 gliosina mo	385	73.5	6.1	380	2	Q6MSB8	Q6MSB8 amycolalops
313	75.5	6.3	275	1	PRXC_PSEST	Q69053 pseudomonas	386	73.5	6.1	386	2	Q6DDJ2	Q6DDJ2 xenopus lae
314	75.5	6.3	427	2	Q9RH76	Q9RH76 alicyclobac	387	73.5	6.1	410	2	Q9CZK0	Q9CZK0 mus musculu
315	75.5	6.3	563	2	Q9IN44	Q9IN44 bovine vira	388	73.5	6.1	426	2	Q83ZV7	Q83ZV7 enterococc
316	75.5	6.3	627	2	Q926L2	Q926L2 listeria in	389	73.5	6.1	463	2	Q6C059	Q6C059 yarrowia li
317	75.5	6.3	634	2	Q8GRU0	Q8GRU0 oryza sativ	390	73.5	6.1	503	1	SHS1_HUMAN	P781324 h proteinc-t
318	75.5	6.3	844	2	Q81767	Q81767 arabidopsis	391	73.5	6.1	593	2	Q8S2E7	Q8S2E7 oryza sativ
319	75.5	6.3	1032	2	Q932929	Q932929 listeria in	392	73.5	6.1	607	2	Q7R3S2	Q7R3S2 giardia lam
320	75.5	6.3	1101	1	PLIG_HUMAN	P46736 homo sapien	393	73.5	6.1	615	2	Q6GNK4	Q6GNK4 xenopus lae
321	75.5	6.3	1102	1	Q9BZC8	Q9BZC8 homo sapien	394	73.5	6.1	635	2	Q96LUR8	Q96LUR8 homo sapien
322	75.5	6.3	1419	2	Q6D375	Q6D375 erwina car	395	73.5	6.1	684	2	Q8EK21	Q8EK21 shewanella
323	75.5	6.3	2035	1	P38A_HUMAN	Q92508 homo sapien	396	73.5	6.1	846	2	Q86W98	Q86W98 homo sapien

397	73.5	6.1	882	2	Q6N5L7	Q6N517	rhodopseudo	470	72	6.0	721	2	Q642N9	Q642n9 xenopus lae
398	73.5	6.1	1044	2	Q94173	Q94173	pneumocysti	471	72	6.0	733	2	Q7PWR1	Q7Pwr1 anopheles g
399	73.5	6.1	1102	2	Q81V23	Q81v23	homo sapien	472	72	6.0	765	2	Q9UVY1	Q9Uvy1 pneumocysti
400	73.5	6.1	1372	2	Q9HAW1	Q9haw1	homo sapien	473	72	6.0	836	2	Q8G5T0	Q8G5t0 oryza sativ
401	73.5	6.1	1388	2	Q9HAW2	Q9haw2	homo sapien	474	72	6.0	984	1	SECA_AQUAE	SECA aquae
402	73.5	6.1	2187	2	Q9H197	Q9h197	homo sapien	475	72	6.0	1051	2	Q6PCR8	Q6Pcr8 mus musculu
403	73.5	6.1	2254	2	Q9HCY0	Q9hcy0	homo sapien	476	72	6.0	1064	2	Q6Z6C4	Q6Z6c4 mus musculu
404	73.5	6.1	2627	2	Q9C0H4	Q9c0h4	homo sapien	477	72	6.0	1085	2	Q811I7	Q811i7 mus musculu
405	73.5	6.1	2627	2	Q869R6	Q869r6	dictyobacte	478	72	6.0	1104	1	STV_YEAST	STV_YEAST
406	73	6.1	155	2	Q67KY3	Q67ky3	dictyobacte	479	72	6.0	1115	2	Q902M5	Q902m5 gallus gall
407	73	6.1	186	2	Q84UX0	Q84ux0	oryza sativ	480	72	6.0	1129	2	Q8PTU5	Q8Ptu5 methanobact
408	73	6.1	255	2	Q6N1M6	Q6n1m6	dictyobacte	481	72	6.0	1482	2	Q6Z0F9	Q6Z0f9 mus musculu
409	73	6.1	287	2	Q8N8P2	Q8n8p2	dictyobacte	482	72	6.0	1674	2	Q86BR4	Q86br4 dictyobacte
410	73	6.1	314	2	Q8N8P2	Q8n8p2	homo sapien	483	72	6.0	1908	2	Q9V8K9	Q9v8k9 dictyobacte
411	73	6.1	314	2	Q8N8P2	Q8n8p2	dictyobacte	484	72	6.0	2087	2	Q86BR6	Q86br6 dictyobacte
412	73	6.1	415	2	Q8V6G3	Q8v6g3	dictyobacte	485	72	6.0	2087	2	Q86BR6	Q86br6 dictyobacte
413	73	6.1	415	2	Q8V6G3	Q8v6g3	dictyobacte	486	72	6.0	184	2	Q9VKI6	Q9vki6 dictyobacte
414	73	6.1	446	2	Q80TC3	Q80tc3	human adeno	487	71.5	5.9	194	2	Q7VKI7	Q7vki7 dictyobacte
415	73	6.1	452	2	Q9SGX8	Q9sgx8	dictyobacte	488	71.5	5.9	258	2	Q92ZG5	Q92zg5 dictyobacte
416	73	6.1	458	2	Q9AET5	Q9aet5	dictyobacte	489	71.5	5.9	289	2	Q72MW9	Q72mw9 dictyobacte
417	73	6.1	458	2	Q9AET5	Q9aet5	dictyobacte	490	71.5	5.9	301	2	Q8EZJ8	Q8ezj8 dictyobacte
418	73	6.1	524	2	Q96W81	Q96w81	dictyobacte	491	71.5	5.9	325	2	Q7NZK1	Q7nzk1 dictyobacte
419	73	6.1	547	2	TX15_HUMAN	TX15_HUMAN	dictyobacte	492	71.5	5.9	334	2	Q9PHW0	Q9phw0 campylobact
420	73	6.1	585	2	Q8TXG6	Q8txg6	dictyobacte	493	71.5	5.9	342	2	Q8RFR9	Q8rfr9 dictyobacte
421	73	6.1	609	2	Q6S1S8	Q6s1s8	dictyobacte	494	71.5	5.9	370	2	Q7MNO1	Q7mno1 dictyobacte
422	73	6.1	614	2	Q8MMA3	Q8mma3	dictyobacte	495	71.5	5.9	392	2	Q9K6B8	Q9k6b8 dictyobacte
423	73	6.1	701	2	Q88XD1	Q88xd1	dictyobacte	496	71.5	5.9	421	2	Q33935	Q33935 dictyobacte
424	73	6.1	747	1	AMD1_HUMAN	AMD1_HUMAN	dictyobacte	497	71.5	5.9	462	2	Q93PB4	Q93pb4 dictyobacte
425	73	6.1	825	2	Q7SHP1	Q7shp1	dictyobacte	498	71.5	5.9	486	2	Q9SCQ0	Q9scq0 dictyobacte
426	73	6.1	825	2	Q6PYB6	Q6pyb6	lemur catia	499	71.5	5.9	513	2	Q6BUI8	Q6bui8 dictyobacte
427	73	6.1	847	2	Q8BFR2	Q8bfr2	m mus muscu	500	71.5	5.9	588	2	Q9PUY5	Q9puY5 dictyobacte
428	73	6.1	847	2	Q8C4T3	Q8c4t3	m mus muscu	501	71.5	5.9	592	2	Q8THB6	Q8thb6 dictyobacte
429	73	6.1	1085	2	Q876N1	Q876n1	dictyobacte	502	71.5	5.9	632	2	Q8D4B6	Q8d4b6 dictyobacte
430	73	6.1	1452	2	Q8UYV8	Q8uyv8	dictyobacte	503	71.5	5.9	649	2	Q9SZK3	Q9szk3 dictyobacte
431	73	6.1	1711	1	PRPV_RAT	PRPV_RAT	dictyobacte	504	71.5	5.9	666	2	Q7S0B3	Q7s0b3 dictyobacte
432	73	6.0	403	2	Q6PKH7	Q6pkh7	homo sapien	505	71.5	5.9	692	2	Q89FD2	Q89fd2 dictyobacte
433	72.5	6.0	403	2	Q6YVE2	Q6yve2	oryza sativ	506	71.5	5.9	725	1	SYM_METAC	SYM_METAC
434	72.5	6.0	403	2	Q6YVE2	Q6yve2	dictyobacte	507	71.5	5.9	725	1	Q9URZ6	Q9urZ6 dictyobacte
435	72.5	6.0	431	2	Q7RXV8	Q7rxv8	dictyobacte	508	71.5	5.9	774	1	FECA_ECOLI	FECA_ECOLI
436	72.5	6.0	437	2	Q9NT57	Q9nt57	dictyobacte	509	71.5	5.9	873	2	Q7ZAH0	Q7zah0 dictyobacte
437	72.5	6.0	447	1	FBX9_HUMAN	FBX9_HUMAN	dictyobacte	510	71.5	5.9	1047	2	Q8YXK0	Q8yxk0 dictyobacte
438	72.5	6.0	513	2	Q64JF3	Q64jf3	dictyobacte	511	71.5	5.9	158	2	Q7VVC2	Q7vvc2 dictyobacte
439	72.5	6.0	644	2	Q31980	Q31980	dictyobacte	512	71	5.9	171	2	Q8NXX4	Q8nxx4 dictyobacte
440	72.5	6.0	644	2	Q31980	Q31980	dictyobacte	513	71	5.9	171	2	Q8NXX4	Q8nxx4 dictyobacte
441	72.5	6.0	667	2	Q7NWK2	Q7nwk2	dictyobacte	514	71	5.9	171	2	Q8NXX4	Q8nxx4 dictyobacte
442	72.5	6.0	1062	2	Q96X97	Q96x97	dictyobacte	515	71	5.9	189	2	Q8Y2K0	Q8y2k0 dictyobacte
443	72.5	6.0	1317	1	PKP4_HUMAN	PKP4_HUMAN	dictyobacte	516	71	5.9	238	2	Q6P3D6	Q6p3d6 dictyobacte
444	72.5	6.0	1317	1	Q6PTG6	Q6ptg6	dictyobacte	517	71	5.9	249	2	Q7Q8W7	Q7q8w7 dictyobacte
445	72.5	6.0	1414	2	Q7S1J1	Q7s1j1	dictyobacte	518	71	5.9	277	2	Q924V3	Q924v3 dictyobacte
446	72.5	6.0	2727	2	Q6NR00	Q6nr00	dictyobacte	519	71	5.9	299	2	Q9DGB0	Q9dgb0 dictyobacte
447	72.5	6.0	2727	2	Q6NR00	Q6nr00	dictyobacte	520	71	5.9	316	2	Q837T2	Q837t2 dictyobacte
448	72	6.0	169	2	Q88ZG3	Q88zg3	dictyobacte	521	71	5.9	329	2	Q8N1R4	Q8n1r4 dictyobacte
449	72	6.0	171	1	YV03_BRAJA	YV03_BRAJA	dictyobacte	522	71	5.9	354	2	Q9D2D9	Q9d2d9 dictyobacte
450	72	6.0	186	2	Q9UTL1	Q9utl1	dictyobacte	523	71	5.9	492	2	Q6AVX4	Q6avx4 dictyobacte
451	72	6.0	186	2	Q9UTL1	Q9utl1	dictyobacte	524	71	5.9	541	2	Q648B9	Q648b9 dictyobacte
452	72	6.0	265	1	HI_PEA	HI_PEA	dictyobacte	525	71	5.9	638	1	Q6KAU0	Q6kau0 dictyobacte
453	72	6.0	270	2	Q9MCA9	Q9mca9	dictyobacte	526	71	5.9	659	1	G1GX_HABIN	G1GX_HABIN
454	72	6.0	276	2	P7J137	P7j137	dictyobacte	527	71	5.9	833	1	CAFA_YERPE	CAFA_YERPE
455	72	6.0	277	2	Q9M5J0	Q9m5j0	dictyobacte	528	71	5.9	860	2	Q9NDT9	Q9ndt9 dictyobacte
456	72	6.0	303	2	Q7ZY42	Q7zy42	dictyobacte	529	71	5.9	989	2	Q7UVE2	Q7uve2 dictyobacte
457	72	6.0	340	2	Q9HX38	Q9hx38	dictyobacte	530	71	5.9	993	2	Q6PLP9	Q6plp9 dictyobacte
458	72	6.0	363	2	Q6CQZ3	Q6cqz3	dictyobacte	531	71	5.9	1004	1	SIPO_BACBR	SIPO_BACBR
459	72	6.0	392	2	Q9HP00	Q9hp00	dictyobacte	532	71	5.9	1048	2	Q7TNT8	Q7tnT8 dictyobacte
460	72	6.0	407	2	Q8BHB3	Q8bhb3	dictyobacte	533	71	5.9	1051	2	Q91XT4	Q91xt4 dictyobacte
461	72	6.0	428	2	Q9RYM5	Q9rym5	dictyobacte	534	71	5.9	1498	2	Q9Y4P5	Q9y4p5 dictyobacte
462	72	6.0	509	2	Q9SBL8	Q9sbl8	dictyobacte	535	71	5.9	1944	1	CHD3_HUMAN	CHD3_HUMAN
463	72	6.0	564	2	Q7S0Z2	Q7s0z2	dictyobacte	536	71	5.9	2000	1	Q9Y4T0	Q9y4t0 dictyobacte
464	72	6.0	600	2	Q9LS72	Q9ls72	dictyobacte	537	70.5	5.9	144	1	RS1A_SCHPO	RS1A_SCHPO
465	72	6.0	602	1	TX15_MOUSE	TX15_MOUSE	dictyobacte	538	70.5	5.9	158	2	Q9F9L6	Q9f9l6 dictyobacte
466	72	6.0	626	1	PPOC_LYCBS	PPOC_LYCBS	dictyobacte	539	70.5	5.9	184	2	Q96CG3	Q96cg3 dictyobacte
467	72	6.0	630	1	PPOA_LYCBS	PPOA_LYCBS	dictyobacte	540	70.5	5.9	237	2	Q58524	Q58524 dictyobacte
468	72	6.0	668	2	Q6NUM6	Q6num6	dictyobacte	541	70.5	5.9	253	2	Q7NKKJ9	Q7nkkj9 dictyobacte
469	72	6.0	691	2	Q87QZ1	Q87qz1	dictyobacte	542	70.5	5.9	280	2	Q9D1C9	Q9d1c9 dictyobacte

543	70.5	5.9	291	2	Q62SF4	Q82sf4	nitrosomona	616	70	5.8	985	2	Q8V05	Q8v05	arabidopsis
544	70.5	5.9	299	2	Q6DAW7	Q6daw7	erwinia car	617	70	5.8	1395	2	Q35059	Q35059	marchantia
545	70.5	5.9	301	2	Q91RL8	Q91rl8	rabies viru	618	70	5.8	2137	2	Q15021	Q15021	homo sapien
546	70.5	5.9	338	2	Q88IC3	Q88ic3	pseudomonas	619	70	5.8	2860	2	Q81640	Q81640	plasmodium
547	70.5	5.9	370	2	Q8DFP7	Q8dfp7	vibrio vuln	620	70	5.8	6797	2	Q9X993	Q9X993	streptomyces
548	70.5	5.9	374	2	Q9LLO7	Q9llq7	vigna ungui	621	70	5.8	204	2	Q87C69	Q87c69	xyella fas
549	70.5	5.9	390	2	Q8UWM1	Q8uwm1	brachydanio	622	70	5.8	215	2	Q716N9	Q716n9	mycobacteri
550	70.5	5.9	392	2	Q6HMB3	Q6hmb3	bellovibri	623	70	5.8	225	1	Y439_PYRHO	Y439_PYRHO	pyrococcus
551	70.5	5.9	398	2	P77842	P77842	chloroflexu	624	70	5.8	259	2	Q86BE4	Q86be4	schistosoma
552	70.5	5.9	423	1	TXB2_CAEEL	P19691	caenorhabdi	625	70	5.8	263	2	Q8MIC5	Q8mic5	cvis arles
553	70.5	5.9	436	2	Q8RTD2	Q8rt02	drosophila	626	70	5.8	268	2	Q74EV9	Q74ev9	geobacteri
554	70.5	5.9	457	2	Q64HY0	Q64hy0	oncorhynch	627	70	5.8	277	2	Q8FAX7	Q8fax7	escherichia
555	70.5	5.9	460	2	Q9FG85	Q9fgh5	arabidopsis	628	70	5.8	291	2	Q6LU44	Q6lu44	photobacter
556	70.5	5.9	507	2	Q9LSJ3	Q9lsj3	arabidopsis	629	70	5.8	312	1	HEM3_VIBVU	Q8dd5	vibrio vuln
557	70.5	5.9	525	2	NCAP_RINDR	Q03332	rinderpest	630	70	5.8	312	2	Q7MOC7	Q7mc7	vibrio vuln
558	70.5	5.9	525	2	Q86381	Q86381	rinderpest	631	70	5.8	327	2	Q7NEA1	Q7neal	gloebacter
559	70.5	5.9	525	2	Q6Z916	Q6z916	rinderpest	632	70	5.8	336	1	VG27_BPML5	Q05234	mycobacteri
560	70.5	5.9	532	1	CAX2_ARATH	Q83998	arabidopsis	633	70	5.8	346	1	AMBP_MERUN	Q62577	meriones un
561	70.5	5.9	606	2	Q751R7	Q751r7	oryza sativ	634	70	5.8	365	2	Q87RP5	Q87rp5	vibrio para
562	70.5	5.9	665	1	GAK3_HUMAN	Q9yna8	homo sapien	635	70	5.8	379	2	Q9HGM1	Q9hgm1	protomyces
563	70.5	5.9	668	2	Q6BWA2	Q6bwa2	debrayomyce	636	70	5.8	389	2	Q9D8Z8	Q9d8z8	mus musculu
564	70.5	5.9	703	2	Q7N905	Q7n9c5	photorhabd	637	70	5.8	391	2	Q75PR0	Q75pr0	physcomitre
565	70.5	5.9	710	1	FOXA_YEREN	Q01674	yersinia en	638	70	5.8	416	2	Q7XK65	Q7xk65	oryza sativ
566	70.5	5.9	792	2	Q7XIG8	Q7xig8	oryza sativ	639	70	5.8	418	2	Q8RTV5	Q8rtv5	lactobacill
567	70.5	5.9	807	2	Q9XFX7	Q9xfx7	craterostig	640	70	5.8	420	2	Q6W970	Q6w970	tenebrio mo
568	70.5	5.9	830	2	FAR1_YEAST	P21268	saccharomyc	641	70	5.8	431	2	Q73V92	Q73v92	mycobacteri
569	70.5	5.9	917	2	Q89KUD	Q89kud	brachyriob	642	70	5.8	456	2	Q9LZ15	Q9lzi5	arabidopsis
570	70.5	5.9	937	2	Q6LLO4	Q6llq4	photobacter	643	70	5.8	462	2	Q9Z506	Q9z506	rhizobium m
571	70.5	5.9	1159	1	K196_HUMAN	Q12768	homo sapien	644	70	5.8	476	2	Q8YU75	Q8yu75	anabaena sp
572	70.5	5.9	1159	1	K196_MOUSE	Q8c2e7	mus musculu	645	70	5.8	492	2	Q9Z5Q2	Q9z5q2	plum sativ
573	70.5	5.9	1298	2	Q6LNT1	Q6lnt1	photobacter	646	70	5.8	525	1	NCAP_RINDU	Q7w92	thermotoga
574	70.5	5.9	1340	2	Q8BEP6	Q8bep6	xanthomonas	647	70	5.8	525	2	Q7WJ92	Q7wj92	rinderpest
575	70.5	5.9	1465	1	YH85_SCHPO	Q9p5n0	schizosacch	648	70	5.8	566	2	Q91N43	Q91n43	bovine vira
576	70.5	5.9	1574	2	Q7Y535	Q7y5j5	xanthomonas	649	70	5.8	588	2	Q835N0	Q835n0	enterococcu
577	70.5	5.9	1734	2	Q8MNL9	Q8mnl9	dicyosteli	650	70	5.8	599	2	Q414Z8	Q414z8	solanum tub
578	70.5	5.9	3914	2	Q70DK0	Q70dk0	bovine vira	651	70	5.8	714	2	Q6B3J3	Q6b3j3	uncultured
579	70.5	5.8	148	2	Q6G1A7	Q6g1q2	bacillus li	652	70	5.8	717	2	Q6P3G5	Q6p3g5	brachydanio
580	70.5	5.8	171	2	Q6G1A7	Q6gia7	staphylococ	653	70	5.8	725	2	Q7VT71	Q7vt71	bordetella
581	70.5	5.8	191	2	Q753H6	Q753h6	ashbya gos	654	70	5.8	725	2	Q7W294	Q7w294	bordetella
582	70.5	5.8	215	1	FGHB_BRARE	Q6ji98	brachydanio	655	70	5.8	725	2	Q7WR61	Q7wr61	bordetella
583	70.5	5.8	257	2	Q8A7H2	Q8a7h2	pleurodeles	656	70	5.8	747	1	AMD1_RAT	AMD1_RAT	retius nori
584	70.5	5.8	270	2	Q6ZML1	Q6zml1	burkholderi	657	70	5.8	754	1	YCA1_ECOLI	YCA1_ECOLI	escherichia
585	70.5	5.8	271	2	Q63X65	Q63x65	burkholderi	658	70	5.8	793	1	AD28_MOUSE	Q9j1i6	mus musculu
586	70.5	5.8	322	2	Q88Q26	Q88q26	sus scrofa	659	70	5.8	811	2	Q6PF55	Q6pf55	xenopus lae
587	70.5	5.8	327	2	Q87W14	Q87w14	pseudomonas	660	70	5.8	840	2	Q9BPV3	Q9bpv3	caenorhabdi
588	70.5	5.8	332	2	Q88DN7	Q88dn7	pseudomonas	661	70	5.8	841	2	Q7USV0	Q7usv0	rhodospirilli
589	70.5	5.8	347	2	Q7WAY1	Q7way1	bordetella	662	70	5.8	857	2	Q74H88	Q74h88	geobacter s
590	70.5	5.8	354	2	Q7MMES	Q7mmes	bordetella	663	70	5.8	910	1	DDHA_RHOSU	Q8p94	rhodovulum
591	70.5	5.8	365	2	Q7VY98	Q7vy98	homo sapien	664	70	5.8	914	2	Q7OY57	Q7oy57	giardia lam
592	70.5	5.8	365	2	Q7VY98	Q6b0v2	bordetella	665	70	5.8	1073	1	ACA9_ARATH	Q91u41	arabidopsis
593	70.5	5.8	368	2	Q6P0V2	Q6p0v2	brachydanio	666	70	5.8	1140	2	Q9P3N7	Q9p3n7	neurospora
594	70.5	5.8	408	2	Q8R2K8	Q8r2k8	homo sapien	667	70	5.8	1250	2	Q82RX1	Q82rx1	streptomyces
595	70.5	5.8	466	1	Q8T4S4	Q8t4s4	aedes aegypt	668	70	5.8	1284	2	Q8RUS1	Q8rus1	neurospora
596	70.5	5.8	466	1	ACM2_CHICK	P30372	gallus gall	669	70	5.8	1456	2	Q8NUS1	Q8nus1	leptospaer
597	70.5	5.8	469	1	YQJ8_CAEEL	P34631	caenorhabdi	670	70	5.8	1481	2	Q693A4	Q693a4	oryza sativ
598	70.5	5.8	474	2	Q89Y07	Q89y07	brachyriob	671	70	5.8	1550	2	Q6WMB9	Q6wmb9	caenorhabdi
599	70.5	5.8	485	2	Q41832	Q41832	zea mays (m	672	70	5.8	1597	2	Q6F0M3	Q6f0m3	drosophila
600	70.5	5.8	518	2	Q88G73	Q88g73	pseudomonas	673	70	5.8	1730	2	Q6R0N8	Q6r0n8	candida gla
601	70.5	5.8	622	2	Q9FG16	Q9fg16	arabidopsis	674	70	5.8	1984	2	Q9QUV4	Q9quv4	viral hemor
602	70.5	5.8	631	2	Q6DV10	Q6dv10	gekkko japon	675	70	5.8	2029	1	IAR_DROME	Q9vi68	drosophila
603	70.5	5.8	647	2	Q9KS43	Q9ks43	vibrio chol	676	70	5.8	2029	2	Q9V1S8	Q9v1s8	geobacteri
604	70.5	5.8	703	2	Q6BYK2	Q6byk2	debrayomyces	677	70	5.8	2270	2	Q9NSJ3	Q9nsj3	homo sapien
605	70.5	5.8	721	2	Q6RYOC	Q6ryoc	xenopus tro	678	70	5.8	3209	2	Q9UTM0	Q9utm0	homo sapien
606	70.5	5.8	743	2	Q6FF05	Q6ff05	actinobact	679	70	5.8	4363	2	Q709E4	Q709e4	homo sapien
607	70.5	5.8	784	2	Q9HXB2	Q9hxb2	pseudomonas	680	70	5.8	4388	2	Q709C5	Q709c5	homo sapien
608	70.5	5.8	801	2	Q6FU33	Q6fu33	candida gla	681	70	5.8	106	2	Q27418	Q27418	methanobact
609	70.5	5.8	809	2	Q7SFF1	Q7sff1	neurospora	682	70	5.8	190	2	Q9SHP3	Q9shp3	arabidopsis
610	70.5	5.8	813	2	Q8W1B2	Q8w1b2	papaver som	683	70	5.8	222	2	Q8BRP4	Q8brp4	mus musculu
611	70.5	5.8	836	2	Q8N394	Q8n394	homo sapien	684	70	5.8	235	2	Q9PGU9	Q9pgu9	xyella fas
612	70.5	5.8	874	2	Q8U1R6	Q8u1r6	brachydanio	685	70	5.8	235	2	Q6DEP7	Q6dep7	brachydanio
613	70.5	5.8	874	2	Q8U1S6	Q8u1s6	brachydanio	686	70	5.8	257	2	Q8ASQ7	Q8asq7	bacteroides
614	70.5	5.8	893	2	Q6S119	Q6s119	uncultured	687	70	5.8	297	2	Q8YQJ8	Q8yqj8	anabaena sp
615	70.5	5.8	983	2	Q8GZ04	Q8gz04	arabidopsis	688	70	5.8	313	2	Q9XS24	Q9xs24	ateles fusc

689	69	5.7	320	2	08XK96	08XK96 clostetridium	762	68.5	5.7	405	2	09A147	09A147 oryza sativ
690	69	5.7	348	2	06TLZ8	06TLZ8 symbiobacte	763	68.5	5.7	419	2	06W978	06W978 diptlopoda s
691	69	5.7	365	2	06ZC68	06ZC68 burkholderi	764	68.5	5.7	419	2	06R824	06R824 streptomyce
692	69	5.7	365	2	06J190	06J190 burkholderi	765	68.5	5.7	420	2	06W971	06W971 harmonia ax
693	69	5.7	365	2	09PW23	09PW23 gallus galli	766	68.5	5.7	425	2	08S9B0	08S9B0 brassica ca
694	69	5.7	368	2	07ZT37	07ZT37 brachydanio	767	68.5	5.7	446	2	09ME76	09ME76 mus musculu
695	69	5.7	378	2	09FH25	09FH25 arabidopsis	768	68.5	5.7	470	2	08W1A1	08W1A1 glycine max
696	69	5.7	403	2	09P5S5	09P5S5 neurospora	769	68.5	5.7	471	2	03S162	03S162 rattus norv
697	69	5.7	415	1	L52_ADE02	P03262 human adeno	770	68.5	5.7	471	2	06IRB1	06IRB1 rattus norv
698	69	5.7	415	2	071BX5	071BX5 human adeno	771	68.5	5.7	502	1	FM02_ORYSA	P92812 oryza sativ
699	69	5.7	415	2	07M6J3	07M6J3 human adeno	772	68.5	5.7	502	2	08HCN7	08HCN7 oryza sativ
700	69	5.7	416	2	08BEV4	08BEV4 shewanella	773	68.5	5.7	508	2	06NH93	06NH93 corynebacte
701	69	5.7	424	2	08LBB2	08LBB2 arabidopsis	774	68.5	5.7	573	2	07MOP8	07MOP8 wolfinella s
702	69	5.7	428	2	093F17	093F17 shigella fl	775	68.5	5.7	573	2	0994B5	0994B5 porcine ade
703	69	5.7	463	2	0874S6	0874S6 aedes aegyp	776	68.5	5.7	575	2	08M2S4	08M2S4 pyrsarum po
704	69	5.7	493	2	071LEP1	071LEP1 betta pugna	777	68.5	5.7	576	2	0648F8	0648F8 uncultured
705	69	5.7	506	1	SHS1_BOVIN	046631 bos taurus	778	68.5	5.7	671	2	07XHY3	07XHY3 oryza sativ
706	69	5.7	522	1	06D2J3	06D2J3 erwina car	779	68.5	5.7	695	2	09SU22	09SU22 arabidopsis
707	69	5.7	527	1	ATRX_RAT	P70486 rattus norv	780	68.5	5.7	705	2	0590S8	0590S8 pyrococcus
708	69	5.7	539	2	09M2B8	09M2B8 arabidopsis	781	68.5	5.7	754	2	082802	082802 salmonella
709	69	5.7	541	2	07M5T4	07M5T4 bordetella	782	68.5	5.7	755	2	07VBL4	07VBL4 prochloroto
710	69	5.7	544	2	07WMD4	07WMD4 bordetella	783	68.5	5.7	761	2	07RYW3	07RYW3 neurospora
711	69	5.7	546	2	06U1O5	06U1Q5 esoc masqui	784	68.5	5.7	812	2	07RWE4	07RWE4 rhodospirell
712	69	5.7	672	2	096NG3	096NG3 homo sapien	785	68.5	5.7	827	2	07UPJ6	07UPJ6 rhodospirell
713	69	5.7	674	2	096SV5	096SV5 homo sapien	786	68.5	5.7	860	2	09ZNM6	09ZNM6 brassica ca
714	69	5.7	686	1	1PR2_MOUSE	09ER66 mus musculu	787	68.5	5.7	873	2	09LS59	09LS59 arabidopsis
715	69	5.7	724	2	06C9H6	06C9H6 yarrowia li	788	68.5	5.7	882	2	09HYV3	09HYV3 pseudomonas
716	69	5.7	733	2	07S1G8	07S1G8 desulfuroco	789	68.5	5.7	948	2	09U3J04	09U3J04 caenorhabdi
717	69	5.7	747	2	098TE7	098TE7 carassius a	790	68.5	5.7	980	2	08A3J1	08A3J1 bacteroides
718	69	5.7	764	2	098UB3	08E1B3 escherichia	791	68.5	5.7	1015	2	06J3U7	06J3U7 yersinia ps
719	69	5.7	773	2	07S1G7	07S1G7 desulfuroco	792	68.5	5.7	1050	2	08CCL4	08CCL4 mus musculu
720	69	5.7	780	2	08XEA2	08XEA2 escherichia	793	68.5	5.7	1059	2	09NBB9	09NBB9 crypanosoma
721	69	5.7	813	2	08WBE9	08WBE9 papaver som	794	68.5	5.7	1096	2	07EZB4	07EZB4 oryza sativ
722	69	5.7	814	2	08TB54	08TB54 homo sapien	795	68.5	5.7	1125	2	093TH9	093TH9 bacteroides
723	69	5.7	815	2	084NP7	084NP7 oryza sativ	796	68.5	5.7	1181	2	06MZY2	06MZY2 homo sapien
724	69	5.7	818	2	08N4X5	08N4X5 homo sapien	797	68.5	5.7	1261	2	06RYO8	06RYO8 asterina mi
725	69	5.7	829	2	08XX81	08XX81 raietonia s	798	68.5	5.7	1609	2	07XTW1	07XTW1 oryza sativ
726	69	5.7	831	2	07RW66	07RW66 neurospora	799	68.5	5.7	2199	2	06DNE5	06DNE5 lymphyra maj
727	69	5.7	834	1	AG01_SCHPO	074957 schizosacch	800	68.5	5.7	3869	2	07WRN5	07WRN5 arabidopsis
728	69	5.7	892	2	P91085	P91085 caenorhabdi	801	68.5	5.7	4307	2	019J19	019J19 caenorhabdi
729	69	5.7	921	2	08SS27	08SS27 encephalito	802	68.5	5.7	5379	2	09FDB3	09FDB3 pseudomonas
730	69	5.7	971	2	0661T8	0661T8 xenopus lae	803	68.5	5.6	153	2	08T601	08T601 eschistosoma
731	69	5.7	1098	2	064719	064719 bos taurus	804	68.5	5.6	183	2	08BPT5	08BPT5 mus musculu
732	69	5.7	1100	2	090WC9	090WC9 mus musculu	805	68.5	5.6	191	2	07J3Z01	07J3Z01 mycobacteri
733	69	5.7	1190	2	068FH0	068FH0 mus musculu	806	68.5	5.6	205	2	091OX8	091OX8 pseudomonas
734	69	5.7	1312	2	08WZV2	08WZV2 neurospora	807	68.5	5.6	224	1	MED2_MOUSE	Q6ECX7 mus musculu
735	69	5.7	1693	2	09P655	09P655 neurospora	808	68.5	5.6	224	2	0483X9	0483X9 klebsiella
736	68.5	5.7	154	2	090Z14	090Z14 xenopus lae	809	68.5	5.6	229	2	08CCX7	08CCX7 mus musculu
737	68.5	5.7	157	1	HS11_DAUCA	P27396 daucus caro	810	68.5	5.6	237	2	08C611	08C611 mus musculu
738	68.5	5.7	164	2	088TD6	088TD6 lactobacill	811	68.5	5.6	253	2	08EXR6	08EXR6 shewanella
739	68.5	5.7	167	2	07NVY0	07NVY0 chromobacte	812	68.5	5.6	277	2	0924V2	0924V2 citreulob
740	68.5	5.7	169	2	0825J0	0825J0 streptomyc	813	68.5	5.6	278	2	08L1J2	08L1J2 oryza sativ
741	68.5	5.7	175	1	COAG_CARRO	P03997 carcinoscor	814	68.5	5.6	290	2	06MDP3	06MDP3 parachlamyd
742	68.5	5.7	188	1	EFPL_XYLPT	087C43 xyella fas	815	68.5	5.6	303	2	0829X2	0829X2 streptomyc
743	68.5	5.7	189	1	EFPL_XYLPA	09qbel xyella fas	816	68.5	5.6	308	2	08T4S5	08T4S5 aedes aegyp
744	68.5	5.7	203	2	07P5G5	07P5G5 fusobacteri	817	68.5	5.6	324	2	08Q0P5	08Q0P5 methanosarc
745	68.5	5.7	203	2	08R1B2	08R1B2 fusobacteri	818	68.5	5.6	332	2	071UV2	071UV2 oryza sativ
746	68.5	5.7	210	2	09VNN5	09VNN5 dirosophila	819	68.5	5.6	332	2	077644	077644 pan troglod
747	68.5	5.7	224	2	09RU88	09RU88 deinococcus	820	68.5	5.6	340	2	087VY0	087VY0 pseudomonas
748	68.5	5.7	239	2	09HMR8	09HMR8 halobacteri	821	68.5	5.6	341	2	07XRA6	07XRA6 oryza sativ
749	68.5	5.7	249	2	064P50	064P50 bacteroides	822	68.5	5.6	342	2	07P6P3	07P6P3 fusobacteri
750	68.5	5.7	262	2	023926	023926 dictyosceli	823	68.5	5.6	352	2	07USC6	07USC6 synecococc
751	68.5	5.7	280	2	08CCR8	08CCR8 mus musculu	824	68.5	5.6	354	2	064BC8	064BC8 uncultured
752	68.5	5.7	298	2	08R257	08R257 mus musculu	825	68.5	5.6	371	2	06GMK4	06GMK4 brachydanio
753	68.5	5.7	304	2	092QY4	092QY4 rhizobium m	826	68.5	5.6	378	2	081BL1	081BL1 arabidopsis
754	68.5	5.7	335	1	06FY90	06FY90 actinosacch	827	68.5	5.6	380	2	08IR27	08IR27 dirosophila
755	68.5	5.7	335	1	YD59_SCHPO	010312 schizosacch	828	68.5	5.6	391	2	09S2B3	09S2B3 streptomyc
756	68.5	5.7	351	2	070P10	070P10 macaca mula	829	68.5	5.6	400	2	086TK5	086TK5 homo sapien
757	68.5	5.7	354	2	091N46	091N46 bovine vita	830	68.5	5.6	403	2	02J3I09	02J3I09 arabidopsis
758	68.5	5.7	355	2	074Z45	074Z45 asbbya goss	831	68.5	5.6	414	2	06PGN5	06PGN5 homo sapien
759	68.5	5.7	374	1	CARA_XYLPA	09pec2 xyella fas	832	68.5	5.6	415	1	L52_ADE05	P04496 human adeno
760	68.5	5.7	405	2	066IK0	066IK0 xenopus tto	833	68.5	5.6	422	2	07M5Z2	07M5Z2 human adeno
761	68.5	5.7	405	2	08TLB6	08TLB6 methanosarc	834	68.5	5.6	422	2	074H55	074H55 geobacter s

835	68	5.6	424	2	Q9S7W6	Q9S7W6	arabidopsis	508	67.5	5.6	306	2	Q8P6N2	Q8P6N2	xanthomonas
836	68	5.6	440	2	Q7V3Y1	Q7V3Y1	prochlorococo	909	67.5	5.6	306	2	Q881S1	Q881S1	pseudomonas
837	68	5.6	442	2	Q9SDP3	Q9SDP3	allium cepa	910	67.5	5.6	319	2	Q9XYQ1	Q9XYQ1	entamoeba h
838	68	5.6	448	2	Q6C4G6	Q6C4G6	varrowia li	911	67.5	5.6	320	2	Q9ZBB0	Q9ZBB0	spingobium
839	68	5.6	449	2	Q9SKN9	Q9SKN9	macaca fasc	912	67.5	5.6	338	2	Q9Z118	Q9Z118	streptomyces
840	68	5.6	449	2	Q9SK03	Q9SK03	arabidopsis	913	67.5	5.6	368	2	Q99PE4	Q99PE4	mus musculus
841	68	5.6	455	2	Q9N134	Q9N134	oryctolagus	914	67.5	5.6	368	2	Q8C7G5	Q8C7G5	mus musculus
842	68	5.6	456	2	Q93CS1	Q93CS1	sigella bo	915	67.5	5.6	369	2	Q9SEK5	Q9SEK5	canavalia l
843	68	5.6	459	2	Q50578	Q50578	pseudomonas	916	67.5	5.6	436	2	Q8GHY5	Q8GHY5	pseudomonas
844	68	5.6	462	2	Q8T4S3	Q8T4S3	aedes aegypt	917	67.5	5.6	383	2	Q8MTN0	Q8MTN0	culicoides
845	68	5.6	463	2	Q8T4S1	Q8T4S1	aedes aegypt	918	67.5	5.6	386	2	Q9RLH5	Q9RLH5	paracoccus
846	68	5.6	463	2	Q8T4S2	Q8T4S2	aedes aegypt	919	67.5	5.6	399	2	Q8R1R1	Q8R1R1	tubobacteri
847	68	5.6	466	2	Q7SXFS	Q7SXFS	brachydanio	920	67.5	5.6	400	2	Q57407	Q57407	xenopus lae
848	68	5.6	475	1	L1PL_HUMAN	L1PL_HUMAN	homo sapien	921	67.5	5.6	436	2	Q8VDY6	Q8VDY6	mus musculus
849	68	5.6	475	1	L1PL_PAPAN	L1PL_PAPAN	papio anubi	922	67.5	5.6	437	2	Q8BK06	Q8BK06	mus musculus
850	68	5.6	475	2	Q61AV0	Q61AV0	homo sapien	923	67.5	5.6	444	2	Q8A5B9	Q8A5B9	bacteroides
851	68	5.6	486	2	Q8XU10	Q8XU10	homo sapien	924	67.5	5.6	453	2	Q6NTH6	Q6NTH6	bacteroides
852	68	5.6	491	2	Q6T6W6	Q6T6W6	stokella a	925	67.5	5.6	454	2	Q9ZEP3	Q9ZEP3	brachydanio
853	68	5.6	506	2	Q8TWB5	Q8TWB5	methanopyru	926	67.5	5.6	472	1	SBPI_MOUSE	SBPI_MOUSE	braasica ju
854	68	5.6	532	2	Q64R32	Q64R32	bacteroides	927	67.5	5.6	472	1	SYTM_MOUSE	SYTM_MOUSE	mus musculus
855	68	5.6	535	2	Q9F1Z5	Q9F1Z5	arabidopsis	928	67.5	5.6	475	2	Q6KAQ6	Q6KAQ6	mus musculus
856	68	5.6	536	2	Q647H4	Q647H4	arachis hyp	929	67.5	5.6	478	2	Q8BP49	Q8BP49	mus musculus
857	68	5.6	538	2	Q8LKN1	Q8LKN1	arachis hyp	930	67.5	5.6	500	2	Q8UJD2	Q8UJD2	porcine lym
858	68	5.6	531	2	Q6E245	Q6E245	neurospora	931	67.5	5.6	501	2	Q6BKX7	Q6BKX7	debaromyces
859	68	5.6	576	2	Q7S4G2	Q7S4G2	neurospora	932	67.5	5.6	512	2	Q54400	Q54400	streptomyces
860	68	5.6	585	2	Q7LICY6	Q7LICY6	homo sapien	933	67.5	5.6	512	2	Q9PJ44	Q9PJ44	streptomyces
861	68	5.6	585	2	Q9UH65	Q9UH65	homo sapien	934	67.5	5.6	513	2	Q6PFL3	Q6PFL3	brachydanio
862	68	5.6	585	2	Q88443	Q88443	mus musculus	935	67.5	5.6	516	2	Q92ZV1	Q92ZV1	lactobacilli
863	68	5.6	585	2	Q6P1D0	Q6P1D0	mus musculus	936	67.5	5.6	532	1	INVA_YEAST	INVA_YEAST	saccharomyces
864	68	5.6	591	2	Q6A028	Q6A028	mus musculus	937	67.5	5.6	550	2	Q8X939	Q8X939	escherichia
865	68	5.6	603	2	Q7S135	Q7S135	homo sapien	938	67.5	5.6	582	2	Q9JY58	Q9JY58	neisseria m
866	68	5.6	670	2	Q9ERJ3	Q9ERJ3	rattus norv	939	67.5	5.6	585	2	Q9JY41	Q9JY41	neisseria m
867	68	5.6	732	2	Q74LC3	Q74LC3	lactobacilli	940	67.5	5.6	595	2	Q88TP0	Q88TP0	lactobacilli
868	68	5.6	762	2	Q9VX06	Q9VX06	dtrosophila	941	67.5	5.6	596	1	PROB_LYCES	PROB_LYCES	lycoperdico
869	68	5.6	848	2	Q83H68	Q83H68	tropheryma	942	67.5	5.6	604	1	KLEI_HUMAN	KLEI_HUMAN	homo sapien
870	68	5.6	876	2	Q74M69	Q74M69	nanorarchaeu	943	67.5	5.6	604	1	KLEI_MOUSE	KLEI_MOUSE	mus musculus
871	68	5.6	876	2	Q83GT6	Q83GT6	tropheryma	944	67.5	5.6	604	1	Q6DFP6	Q6DFP6	xenopus lae
872	68	5.6	893	2	Q8KPV2	Q8KPV2	mycobacteri	945	67.5	5.6	620	2	TYRO_NEUCR	TYRO_NEUCR	neurospora
873	68	5.6	1021	2	Q06342	Q06342	mycobacteri	946	67.5	5.6	642	1	Q6CSY1	Q6CSY1	kluyveromyces
874	68	5.6	1041	2	Q6AE19	Q6AE19	leifsonia x	947	67.5	5.6	663	2	Q7RVU7	Q7RVU7	neurospora
875	68	5.6	1056	2	Q8S7A6	Q8S7A6	oryza sativ	948	67.5	5.6	667	2	Q6R7E4	Q6R7E4	ostreid hez
876	68	5.6	1056	2	Q7XFM6	Q7XFM6	oryza sativ	949	67.5	5.6	679	2	Q67K46	Q67K46	syndibacte
877	68	5.6	1075	2	Q7D5G6	Q7D5G6	mycobacteri	950	67.5	5.6	685	2	Q6MGJ7	Q6MGJ7	neurospora
878	68	5.6	1085	2	Q6CB00	Q6CB00	varrowia li	951	67.5	5.6	706	2	Q12296	Q12296	saccharomyces
879	68	5.6	1136	2	Q8K2V0	Q8K2V0	mus musculus	952	67.5	5.6	754	2	P70847	P70847	lactobacilli
880	68	5.6	1157	1	XYNA_THESA	P36917	thermoanaer	953	67.5	5.6	763	2	Q9FKG5	Q9FKG5	arabidopsis
881	68	5.6	1173	2	Q63624	Q63624	rattus norv	954	67.5	5.6	860	2	Q6SVR5	Q6SVR5	mannheimia
882	68	5.6	1304	2	Q9CMP6	Q9CMP6	pasteurella	955	67.5	5.6	894	2	Q6PGK0	Q6PGK0	mus musculus
883	68	5.6	1523	1	DPOL_THERM	P74918	thermococcu	956	67.5	5.6	1004	2	Q8CGA7	Q8CGA7	mus musculus
884	68	5.6	1524	2	Q9V854	Q9V854	dtrosophila	957	67.5	5.6	1008	2	Q7PO53	Q7PO53	anopheles g
885	68	5.6	1866	1	SBPI_HUMAN	Q95248	homo sapien	958	67.5	5.6	1010	1	HCS8_MOUSE	HCS8_MOUSE	mus musculus
886	68	5.6	2266	1	POLI_TBRYM	Q888X3	l rnal poly	959	67.5	5.6	1023	2	Q6PAE7	Q6PAE7	mus musculus
887	68	5.6	2476	1	ZAN_PIG	Q28983	sus scrofa	960	67.5	5.6	1034	2	Q8VHL7	Q8VHL7	mus musculus
888	68	5.6	5412	2	Q7R3N4	Q7R3N4	glardia lam	961	67.5	5.6	1034	2	Q8VHL7	Q8VHL7	mus musculus
889	67.5	5.6	122	2	Q7Z2A2	Q7Z2A2	listeria mae	962	67.5	5.6	1050	2	Q7S1N5	Q7S1N5	neurospora
890	67.5	5.6	154	2	Q7ZYL8	Q7ZYL8	xenopus lae	963	67.5	5.6	1058	2	Q873P1	Q873P1	emeritella
891	67.5	5.6	168	1	YXKA_BACSU	P55185	bacillus su	964	67.5	5.6	1082	1	NCO3_RAT	NCO3_RAT	rattus norv
892	67.5	5.6	188	2	Q6WZB8	Q6WZB8	rhizobium s	965	67.5	5.6	1118	2	Q8KVT1	Q8KVT1	uncultured
893	67.5	5.6	204	2	Q9PBH4	Q9PBH4	xyella fas	966	67.5	5.6	1242	2	Q8XRI5	Q8XRI5	raistrontia s
894	67.5	5.6	231	2	Q73EC6	Q73EC6	bacillus ce	967	67.5	5.6	1247	2	Q700S6	Q700S6	anopheles g
895	67.5	5.6	236	2	Q8U895	Q8U895	agrobacteri	968	67.5	5.6	1407	1	RPOC_XYLFA	RPOC_XYLFA	xyella fas
896	67.5	5.6	236	2	Q8KXU3	Q8KXU3	mus musculus	969	67.5	5.6	1407	1	RPOC_XYLFT	RPOC_XYLFT	xyella fas
897	67.5	5.6	247	2	Q6FYX0	Q6FYX0	bartonella	970	67.5	5.6	1673	2	Q6MWC6	Q6MWC6	oryza sativ
898	67.5	5.6	259	2	Q9DSK1	Q9DSK1	m mus muscu	971	67.5	5.6	1726	2	Q7WKT6	Q7WKT6	borderella
899	67.5	5.6	265	2	Q9XYF5	Q9XYF5	hydra atren	972	67.5	5.6	1729	2	Q7W7E7	Q7W7E7	borderella
900	67.5	5.6	270	2	Q7QSS0	Q7QSS0	glardia lam	973	67.5	5.6	1939	2	Q8TKB8	Q8TKB8	methanosarc
901	67.5	5.6	271	1	Q7NDV1	Q7NDV1	gloeobacter	974	67.5	5.6	1984	2	Q9OBH1	Q9OBH1	viral hemor
902	67.5	5.6	289	2	Y056_MYCGB	P43302	mycoplasma	975	67.5	5.6	1984	2	Q9OBH5	Q9OBH5	viral hemor
903	67.5	5.6	289	2	Q63CB5	Q63CB5	bacillus ce	976	67.5	5.6	1984	2	Q9QJW0	Q9QJW0	vital hemor
904	67.5	5.6	289	2	Q73919	Q73919	bacillus ce	977	67.5	5.6	3988	2	Q8TP21	Q8TP21	methanosarc
905	67.5	5.6	291	1	YF92_SYNN3	P72970	synecocyst	978	67	5.6	41	2	Q9QVZ3	Q9QVZ3	rattus sp.
906	67.5	5.6	295	2	Q8S7P0	Q8S7P0	oryza sativ	979	67	5.6	104	2	Q8DLR9	Q8DLR9	synecococc
907	67.5	5.6	299	1	PUR7_STRAW	Q83FV6	streptomyces	980	67	5.6	110	2	Q7X5E5	Q7X5E5	erwinia rha

981	67	5.6	145	2	Q831V4	Q831v4 shigella fl	1054	67	5.6	812	1	PDAL_MAIZE	Q43270 zea mays (m
982	67	5.6	151	2	Q63X36	Q63x36 burkholderi	1055	67	5.6	814	2	Q87V08	Q8cdu0 mus musculus
983	67	5.6	157	1	RSVR_COTJA	P19162 coturnix co	1056	67	5.6	829	2	Q8CDN0	Q44207 agrobacteri
984	67	5.6	158	1	YBHB_ECOLI	P12994 escherichia	1057	67	5.6	841	2	Q44207	Q82c65 streptomyces
985	67	5.6	158	2	Q71HP4	Q71hp4 escherichia	1058	67	5.6	857	2	Q82CP5	Q6cb57 yarrowia li
986	67	5.6	158	2	Q9AP3	Q9ap3 uncultured	1059	67	5.6	967	2	Q6CB57	Q75gm6 oryza sativ
987	67	5.6	158	2	Q82895	Q82895 salmonella	1060	67	5.6	1614	2	Q75GM6	Q7qgd8 giardia lam
988	67	5.6	158	2	Q82Q08	Q82q08 salmonella	1061	67	5.6	1661	2	Q7QOD8	Q8aw45 plasmodium
989	67	5.6	158	2	Q7UD98	Q7ud98 shigella fl	1062	67	5.6	1766	2	Q8AW45	Q8ic45 mycobacteri
990	67	5.6	158	2	Q8FJQ8	Q8fjq8 escherichia	1063	67	5.6	2201	2	Q81FQ5	Q8xc42 mycobacteri
991	67	5.6	158	2	Q8X828	Q8x828 escherichia	1064	67	5.6	2552	2	Q9XCP2	Q7d717 mycobacteri
992	67	5.6	205	1	RS7_HALMA	P13552 haloarcula	1065	67	5.6	4151	2	Q7D717	Q53490 mycobacteri
993	67	5.6	218	2	Q7VDM6	Q7vwm6 bordetella	1066	67	5.6	4151	2	Q53490	Q7ves2 mycobacteri
994	67	5.6	218	2	Q7M3Z9	Q7m3z9 bordetella	1067	67	5.6	4151	2	Q7VES2	Q42776 zygosacchar
995	67	5.6	218	2	Q7MFD1	Q7mfd1 bordetella	1068	67	5.6	164	2	Q42776	Q8pe01 xanthomonas
996	67	5.6	219	2	Q9L656	Q9l956 oryza sativ	1069	66.5	5.5	203	2	Q8PE01	P95335 myxococcus
997	67	5.6	242	2	Q29153	Q29153 vulpes vulp	1070	66.5	5.5	240	2	P95335	Q72t63 leptospira
998	67	5.6	260	2	Q6MYB7	Q6myb7 aspergillus	1071	66.5	5.5	243	2	Q72TR3	Q8f1y1 leptospira
999	67	5.6	274	2	Q8RIN3	Q8rin3 escherichia	1072	66.5	5.5	244	2	Q8F1Y1	Q69hs2 ctiona intes
1000	67	5.6	274	2	Q8X8G6	Q8x8g6 escherichia	1073	66.5	5.5	276	2	Q69HS2	Q6f1a2 actinobact
1001	67	5.6	277	2	Q7UT29	Q7ut29 rhodospirell	1074	66.5	5.5	281	2	Q6FPA2	Q9ugb7 homo sapien
1002	67	5.6	290	2	Q752M4	Q752m4 ashdya goss	1075	66.5	5.5	285	2	Q967F6	Q867b6 gnathotrupe
1003	67	5.6	305	1	SYGA_VIBCH	Q9kvw7 vibrio chol	1076	66.5	5.5	285	2	Q813M9	Q813m9 bacillus ce
1004	67	5.6	311	2	Q9K6W3	Q9k6w3 bacillus ha	1077	66.5	5.5	289	2	Q45090	Q45090 burkholderi
1005	67	5.6	320	2	Q83YR4	Q83yr4 streptococc	1078	66.5	5.5	297	2	Q45090	Q7ax06 neisseria m
1006	67	5.6	321	2	Q68CY2	Q68cy2 homo sapien	1079	66.5	5.5	309	2	Q7AX06	Q9jir9 neisseria m
1007	67	5.6	346	2	Q9X1R1	Q9x1r1 thermotoga	1080	66.5	5.5	309	2	Q9JIR9	Q9a1a1 sphingomona
1008	67	5.6	348	2	Q19PG1	Q19pg1 gonostoma g	1081	66.5	5.5	320	2	Q9A1S1	Q7xt82 oryza sativ
1009	67	5.6	361	2	Q19635	Q19635 caenorhabdi	1082	66.5	5.5	326	2	Q7XT82	Q8k7u2 streptococc
1010	67	5.6	367	2	Q9KTE1	Q9kte1 vibrio chol	1083	66.5	5.5	328	1	Y630_STRP3	Q67332 streptococc
1011	67	5.6	369	2	Q6K1Z1	Q6k1z1 oryza sativ	1084	66.5	5.5	328	1	Y915_STRPY	Q67332 streptococc
1012	67	5.6	372	1	CDK9_HUMAN	P50750 homo sapien	1085	66.5	5.5	328	1	Y973_STRP8	Q67333 streptococc
1013	67	5.6	387	2	Q6TNI9	Q6tni9 nicotiana b	1086	66.5	5.5	328	1	YB34_STRAS	Q67338 streptococc
1014	67	5.6	389	2	Q9LFT1	Q9lft1 arabidopsis	1087	66.5	5.5	328	1	YF04_STRAS	Q7lkw5 anopheles g
1015	67	5.6	396	2	Q9SDZ5	Q9sdz5 oryza sativ	1088	66.5	5.5	330	2	Q7QEW5	Q7lkw5 schistosach
1016	67	5.6	400	2	Q89N13	Q89n13 bradyrhizob	1089	66.5	5.5	346	2	Q7LKK7	Q6c7h2 yarrowia li
1017	67	5.6	403	2	Q9U250	Q9u250 caenorhabdi	1090	66.5	5.5	354	2	Q6C7H2	Q6rd34 thermoaer
1018	67	5.6	407	2	Q8BS18	Q8bs18 mus musculu	1091	66.5	5.5	355	2	Q8RD34	Q91x90 mus musculu
1019	67	5.6	407	2	Q8CGV1	Q8cgv1 mus musculu	1092	66.5	5.5	368	2	Q91X90	Q9p847 splimycos
1020	67	5.6	412	1	LYA3_HUMAN	Q8nc3 mus musculu	1093	66.5	5.5	387	2	Q9P847	P27501 rice tungro
1021	67	5.6	431	1	TRPB_DEIRA	Q9rcv1 deinococcus	1094	66.5	5.5	389	1	YP46_RTBPV	Q9y6a7 homo sapien
1022	67	5.6	458	2	Q9RHAS	Q9rhas pseudomonas	1095	66.5	5.5	391	2	Q9Y6S7	Q91lrl arabidopsis
1023	67	5.6	459	2	Q747H0	Q747h0 geobacter s	1096	66.5	5.5	402	2	Q91LR1	P12031 helix pomat
1024	67	5.6	465	1	APR1_ARATH	P92979 a 5'-adenyl	1097	66.5	5.5	410	1	HCYB_HELPO	Q89g99 bradyrhizob
1025	67	5.6	465	2	Q8LA60	Q8la60 arabidopsis	1098	66.5	5.5	412	2	Q89G99	Q7up54 rhodospirell
1026	67	5.6	474	1	L1PL_RAT	Q06000 rattus norv	1099	66.5	5.5	418	2	Q7UP54	Q9sadi arabidopsis
1027	67	5.6	478	1	L1PL_FELCA	P55031 felis silve	1100	66.5	5.5	429	2	Q9SAD0	Q6atk7 oryza sativ
1028	67	5.6	484	2	Q8PAP4	Q8pap4 xanthomonas	1101	66.5	5.5	442	2	Q6ATK7	Q8uuno gallus gall
1029	67	5.6	488	2	Q7QJ10	Q7qj10 anopheles g	1102	66.5	5.5	451	2	Q8UUN0	Q96bhl homo sapien
1030	67	5.6	493	2	Q83S84	Q83s84 shigella fl	1103	66.5	5.5	459	1	RN25_HUMAN	Q7sh43 neurospora
1031	67	5.6	497	2	Q6LKY2	Q6lky2 photobacter	1104	66.5	5.5	487	2	Q7SHA3	Q9hs93 halobacteri
1032	67	5.6	505	1	MAJ3_DROME	P07192 drosophila	1105	66.5	5.5	495	1	GATB_HALM1	Q7qeb9 giardia lam
1033	67	5.6	556	2	Q6U1Q2	Q6u1q2 novumpra hu	1106	66.5	5.5	528	1	Q7QTE9	P10594 saccharomyc
1034	67	5.6	556	2	Q53641	Q53641 sulfolobus	1107	66.5	5.5	532	1	INV1_YEAST	Q6h960 saccharomyc
1035	67	5.6	567	1	TPA3_MOUSE	Q60803 mus musculu	1108	66.5	5.5	532	2	Q6H9E0	Q65c72 saccharomyc
1036	67	5.6	568	1	TRA3_HUMAN	Q13114 homo sapien	1109	66.5	5.5	532	2	Q65C72	Q65c73 saccharomyc
1037	67	5.6	571	1	V036_FOWPY	Q9j5c4 fowlpox vir	1110	66.5	5.5	532	2	Q65C73	Q6ul66 esox lucius
1038	67	5.6	571	2	Q7OH58	Q7oh58 debrayomyce	1111	66.5	5.5	546	2	Q6U1Q6	Q8p1c8 methanosaarc
1039	67	5.6	619	2	Q6B1U3	Q76616 neurospora	1112	66.5	5.5	583	2	Q8PTC8	Q829a8 streptomyc
1040	67	5.6	632	2	Q68616	Q68x68 rickettsia	1113	66.5	5.5	608	2	Q829A8	Q9QMW7 rattus norv
1041	67	5.6	635	2	Q68X68	Q68x68 rickettsia	1114	66.5	5.5	611	2	Q9QMW7	Q33838 thermotoga
1042	67	5.6	678	1	CAN9_RAT	Q93920 rattus norv	1115	66.5	5.5	611	2	Q33838	Q6f860 actinobact
1043	67	5.6	678	1	MPH1_SCHPO	Q94235 schizosacch	1116	66.5	5.5	637	2	Q94235	Q8bwb1 xanthomonas
1044	67	5.6	691	2	Q7ZU98	Q7zu98 brachydanio	1117	66.5	5.5	639	2	Q955X2	Q9qub7 te virtus o
1045	67	5.6	728	2	Q8B1D1	Q8b1d1 m mus muscu	1118	66.5	5.5	640	2	Q6F860	Q9jxj3 neisseria m
1046	67	5.6	732	2	Q9NV66	Q9nv66 homo sapien	1119	66.5	5.5	649	2	Q8PBW1	Q8j7f6 clostridium
1047	67	5.6	737	1	DEP3_HUMAN	Q9ny33 homo sapien	1120	66.5	5.5	720	2	Q9DUB7	Q95d65 caenorhabdi
1048	67	5.6	751	1	Q7ZU06	Q7zu06 brachydanio	1121	66.5	5.5	725	2	Q9JUX3	Q95d65 caenorhabdi
1049	67	5.6	753	2	Q6ZS84	Q6zsb4 homo sapien	1122	66.5	5.5	790	1	Q20599	Q95d65 caenorhabdi
1050	67	5.6	753	2	Q9OWS1	Q9ows1 fugu rubrip	1123	66.5	5.5	793	1	SYFB_CLOPE	Q95d65 caenorhabdi
1051	67	5.6	769	2	Q8K2G0	Q8k2g0 mus musculu	1124	66.5	5.5	842	2	Q95OF5	Q95d65 zimnia eleg
1052	67	5.6	793	2	Q92819	Q92819 listeria in	1125	66.5	5.5	848	2	Q8H962	Q95d65 zimnia eleg
1053	67	5.6	804	2	Q8N885	Q8n885 homo sapien	1126	66.5	5.5	849	2	Q8VX29	Q9vxx2 zimnia eleg

1127	66.5	5.5	956	1	CYLD_HUMAN	09qnc7	homo sapien	1200	66	5.5	493	1	YBGM_ECOLI	P75742	escherichia
1128	66.5	5.5	963	2	O9LS91	Q91891	arabidopsis	1201	66	5.5	493	2	O9N869	Q9n889	plasmodium
1129	66.5	5.5	964	2	O7SEB3	Q75eg3	asbhyia goss	1202	66	5.5	493	2	O7AGL2	Q7ag12	escherichia
1130	66.5	5.5	973	2	O86728	O86728	streptomyce	1203	66	5.5	493	2	O8X9D3	O8x9d3	escherichia
1131	66.5	5.5	1030	2	O875U4	O875U4	saccharomyce	1204	66	5.5	501	2	O81GP1	O81gp1	arabidopsis
1132	66.5	5.5	1031	2	O80YN7	O80YN7	mus musculus	1205	66	5.5	501	2	O6NV47	O6nv47	mus musculus
1133	66.5	5.5	1047	2	O6C109	O6C109	yarrowia li	1206	66	5.5	501	2	O8C8B2	O8c8b2	mus musculus
1134	66.5	5.5	1064	1	CARB_LACLC	O88464	zea mays (m	1208	66	5.5	501	2	O8CAL3	O8ca13	mus musculus
1135	66.5	5.5	1066	1	O88464	O88464	zea mays (m	1209	66	5.5	501	2	O8CBW4	O8cbw4	mus musculus
1136	66.5	5.5	1077	1	CARB_VIBPA	O80ux0	mus musculus	1210	66	5.5	502	2	O8CBX8	O8cbx8	mus musculus
1137	66.5	5.5	1129	2	O80UFO	O80ux0	mus musculus	1210	66	5.5	502	2	O8CBX8	O8cbx8	mus musculus
1138	66.5	5.5	1179	2	O9N8M4	O9n8m4	trypanosoma	1211	66	5.5	507	2	O8P5H0	O8p5h0	xanthomonas
1139	66.5	5.5	1305	2	O7P5NS	O7p5ns	anopheles g	1212	66	5.5	520	2	O8UFT3	O8uft3	agrobacteri
1140	66.5	5.5	1336	2	O9ESH4	O9esh4	mus musculus	1213	66	5.5	528	2	O6K7L3	O6k7l3	oryza sativ
1141	66.5	5.5	1341	2	O9J1ES	O9j1es	leishmania	1214	66	5.5	544	2	O9NUL8	O9nul8	homo sapien
1142	66.5	5.5	1392	1	CND1_MOUSE	O8K2z4	mus musculus	1215	66	5.5	547	2	O7CZB0	O7czb0	agrobacteri
1143	66.5	5.5	1397	2	O6ZQ1L	O6zq1l	mus musculus	1216	66	5.5	560	2	O9H8A6	O9h8a6	homo sapien
1144	66.5	5.5	1426	2	O6ZGV8	O6zgv8	oryza sativ	1217	66	5.5	561	2	O9H9C4	O9h9c4	homo sapien
1145	66.5	5.5	1455	2	O6ZPU4	O6zpu4	mus musculus	1218	66	5.5	574	2	O9V4T8	O9v4t8	drosophila
1146	66.5	5.5	1561	2	O924D2	O924d2	mus musculus	1219	66	5.5	591	2	O6ABN3	O6abn3	leishmania
1147	66.5	5.5	1578	2	O616G8	O616g8	mus musculus	1220	66	5.5	592	2	O6MKJ7	O6mkj7	bellovibri
1148	66.5	5.5	1717	2	O7PFP8	O7pff8	anopheles g	1221	66	5.5	593	2	O7SPQ7	O7spq7	neurospora
1149	66.5	5.5	1940	2	O6PDM3	O6pdn3	mus musculus	1222	66	5.5	607	2	O74ZC8	O74zc8	asbhyia goss
1150	66.5	5.5	1950	2	O80YN8	O80yn8	mus musculus	1223	66	5.5	635	1	SYT_RICPR	O05947	tickectara
1151	66.5	5.5	2193	2	O9DY01	O9dy01	human enter	1224	66	5.5	638	2	O9Z3B9	O9z3b9	streptomyce
1152	66.5	5.5	2193	2	O9DY02	O9dy02	human enter	1225	66	5.5	642	2	O8BER9	O8ber9	shewanella
1153	66.5	5.5	2193	2	O9QF52	O9qf52	human enter	1226	66	5.5	647	1	CN16_SALTY	P26265	salmonella
1154	66.5	5.5	2193	2	O9QRL8	O9qrl8	human enter	1227	66	5.5	654	2	O989X2	O989x2	rhizobium l
1155	66.5	5.5	2193	2	O9QRL8	O9qrl8	human enter	1227	66	5.5	654	2	O989X2	O989x2	rhizobium l
1156	66.5	5.5	2193	2	O9QRL8	O9qrl8	human enter	1228	66	5.5	654	2	O989X2	O989x2	rhizobium l
1157	66.5	5.5	2193	2	O9QRL8	O9qrl8	human enter	1229	66	5.5	665	1	GAK2_HUMAN	O77id9	homo sapien
1158	66.5	5.5	2858	1	O81AK2	O81ak2	plasmodium	1230	66	5.5	665	1	GAK5_HUMAN	P26684	homo sapien
1159	66.5	5.5	3358	1	PGCV_MOUSE	O62059	mus musculus	1231	66	5.5	680	2	O6MYU6	O6myu6	aspergillus
1160	66.5	5.5	124	2	O6AMX8	O6amx8	desulfotale	1232	66	5.5	692	2	O8NZ02	O8nzz2	anabaena sp
1161	66.5	5.5	160	2	O8C2Z4	O8c2z4	mus musculus	1233	66	5.5	702	2	O8NDB8	O8ndb8	homo sapien
1162	66.5	5.5	169	2	O8CVN3	O8cvn3	escherichia	1234	66	5.5	706	1	MR11_RAT	O9jimo	rettus norv
1163	66.5	5.5	186	1	THM2_ARATH	O9seu8	arabidopsis	1235	66	5.5	712	2	O7XBB0	O7xbb0	oryza sativ
1164	66.5	5.5	210	2	O7OJCS	O83zr7	corynebacte	1236	66	5.5	716	2	O71EB0	O71e60	agrobacteri
1165	66.5	5.5	219	2	O819E7	O7ofcs	bacillus li	1237	66	5.5	717	2	O9QPI8	O9qp18	gallid harp
1166	66.5	5.5	226	2	O9KYV0	O819e7	bacillus ce	1238	66	5.5	738	1	PLAP_HUMAN	O9Y263	homo sapien
1167	66.5	5.5	238	2	O67863	O9kyv0	streptomyce	1239	66	5.5	738	2	O83TK7	O83tk7	streptomyce
1168	66.5	5.5	247	2	O7NEA7	O67863	aquilex aeo	1240	66	5.5	751	2	O8AIV4	O8aiv4	brachydanio
1169	66.5	5.5	256	2	O9X6R7	O7neat	gloeobacter	1241	66	5.5	770	2	O49846	O49846	egeria dens
1170	66.5	5.5	262	2	O7Q7Q1	O9x6r7	streptomyce	1242	66	5.5	775	2	DPOL_THES9	O6366	thermococcu
1171	66.5	5.5	263	2	O96RNF	O7q7q1	anophelies g	1243	66	5.5	776	2	O9SH68	O9sh68	arabidopsis
1172	66.5	5.5	276	2	O7MAZ9	O96rn6	homo sapien	1244	66	5.5	779	2	O831Q3	O831q3	enterococcu
1173	66.5	5.5	296	2	O8NBR1	O7maz9	botdeterlia	1245	66	5.5	795	2	O9NVE3	O9nve3	homo sapien
1174	66.5	5.5	304	2	O9RPJ7	O8nbt1	homo sapien	1246	66	5.5	795	2	O9UE53	O9ue53	homo sapien
1175	66.5	5.5	309	2	O6CUC3	O9rpj7	sphingopyxi	1247	66	5.5	939	1	O64XK8	O64xk8	bacterioides
1176	66.5	5.5	311	2	O8YF20	O6cuk3	kluyveromyc	1248	66	5.5	1005	1	EVC_MOUSE	P57680	mus musculu
1177	66.5	5.5	337	2	O64WF2	O8yp20	anabaena sp	1249	66	5.5	1042	2	O555Z8	O555z8	synechocyst
1178	66.5	5.5	350	2	O8YRBE	O64wf2	bacterioides	1250	66	5.5	1065	2	O7TVU1	O7tvu1	mycobacteri
1179	66.5	5.5	361	2	O64WS3	O8yrb6	anabaena sp	1251	66	5.5	1077	2	O8TE71	O8te71	homo sapien
1180	66.5	5.5	375	2	O8RFJ35	O64ws3	bacterioides	1252	66	5.5	1078	2	O9AJ3U0	O9aj3u0	caulobacter
1181	66.5	5.5	380	2	O6NZT4	O8fj35	escherichia	1253	66	5.5	1095	2	O913U4	O913u4	pseudomonas
1182	66.5	5.5	381	2	O84G12	O6nz4	brachydanio	1254	66	5.5	1098	2	O75BP5	O75bp5	asbhyia goss
1183	66.5	5.5	381	2	O84G13	O84g12	enterobacte	1255	66	5.5	1126	2	O6IMN5	O6imn5	homo sapien
1184	66.5	5.5	395	2	O7QWQ4	O84g13	enterobacte	1256	66	5.5	1127	2	O6IMN6	O6imn6	homo sapien
1185	66.5	5.5	401	1	CAPA_AGRYS	O70wq4	thermoprote	1257	66	5.5	1189	2	O6C867	O6c867	yarrowia li
1186	66.5	5.5	420	2	O6C831	O8udf7	agrobacteri	1258	66	5.5	1194	2	O9R6F0	O9r6f0	agrobacteri
1187	66.5	5.5	423	2	O820X2	O6c831	yarrowia li	1259	66	5.5	1391	2	O72XT3	O72xt3	xenopus lae
1188	66.5	5.5	423	2	O82JZ5	O8xjz5	salmonella	1261	66	5.5	1495	2	O94CX4	O94cx4	oryza sativ
1189	66.5	5.5	443	2	O9HAI4	O9hai4	homo sapien	1262	66	5.5	1520	2	O15829	O15829	leishmania
1190	66.5	5.5	455	2	O8A354	O8a354	bacterioides	1263	66	5.5	1613	2	O9N1B0	O9n1b0	trypanosoma
1191	66.5	5.5	457	2	O6PHD9	O8dhd9	brachydanio	1264	66	5.5	1713	2	O9VRG4	O9vrg4	drosophila
1192	66.5	5.5	462	2	O8EBH9	O8ebh9	drosophila	1265	66	5.5	2089	2	O39478	O39478	cycloctella
1193	66.5	5.5	466	2	O9USN2	O9usn2	schizosacch	1266	66	5.5	2311	1	O6DNF2	O6dnf2	lynghya maj
1194	66.5	5.5	471	2	O648A5	O648a5	uncultured	1267	66	5.5	2326	1	PGG2_RAT	O00657	rattus norv
1195	66.5	5.5	475	2	O96FC4	O96fc4	homo sapien	1268	66	5.5	2462	2	O7Q7Q3	O7q7q3	giardia lam
1196	66.5	5.5	475	2	O949Y3	O949y3	arabidopsis	1269	66	5.5	2478	2	O8YTN5	O8ytn5	anabaena sp
1197	66.5	5.5	476	2	O7P6P1	O7p6p1	anopheles g	1270	66	5.5	2834	2	O20456	O20456	caenorhabdi
1198	66.5	5.5	477	2	O96JF4	O96jf4	homo sapien	1271	66	5.5	3068	1	POLG_PENVC	O01500	p genome po
1199	66.5	5.5	479	2	O8H3X8	O8h3x8	oryza sativ	1272	66	5.5	3068	2	O8JRK5	O8jrk5	pepper motc

1273	66	5.5	3472	2	Q632D5	Q632d5 bacillus ce	1346	65.5	5.4	594	2	Q8PS07	Q8psq7 methanoarc
1274	65.5	5.4	122	2	Q8ZUF9	Q8z1f9 yersinia pe	1347	65.5	5.4	616	2	Q6ATV3	Q6atv3 oryza sativ
1275	65.5	5.4	124	2	YE22_RHME	Q92qb2 rhizobium m	1348	65.5	5.4	631	2	Q6UAN4	Q6uan4 tetradon n
1276	65.5	5.4	136	2	Q664L7	Q664l7 yersinia ps	1349	65.5	5.4	643	1	SYT_PASMU	SYT857 pasteurella
1277	65.5	5.4	142	2	Q8CK96	Q8ck96 yersinia pe	1350	65.5	5.4	646	2	Q7RAD3	Q7rad3 giardia lam
1278	65.5	5.4	151	2	Q63109	Q63109 burkholderi	1351	65.5	5.4	646	2	Q810E8	Q810e8 oryza sativ
1279	65.5	5.4	159	1	HS12_DAUCA	P27397 daucus caro	1352	65.5	5.4	664	2	Q911W4	Q911w4 pseudomonas
1280	65.5	5.4	161	2	Q9HJ86	Q9hj86 thermoplas	1353	65.5	5.4	670	1	DN1J_BACST	DN1j bacillus st
1281	65.5	5.4	169	2	Q8DST0	Q8dst0 streptococc	1354	65.5	5.4	709	2	Q9R279	Q9r279 deinococcus
1282	65.5	5.4	179	2	Q938C7	Q938c7 mycobacteri	1355	65.5	5.4	715	1	DCB1_HUMAN	Q8nz78 homo sapien
1283	65.5	5.4	195	1	COAG_LIMPO	P03998 limulus pol	1356	65.5	5.4	716	2	Q8RSF8	Q8rsf8 mus musculu
1284	65.5	5.4	198	1	LOLA_VIBVY	Q7m1v4 vibrio vuln	1357	65.5	5.4	756	2	Q8DXK1	Q8dxk1 synechococc
1285	65.5	5.4	199	2	Q881E2	Q881e2 pseudomonas	1358	65.5	5.4	763	2	Q7QTM4	Q7qtm4 giardia lam
1286	65.5	5.4	199	2	Q9D1X5	Q9d1x5 m mus muscu	1359	65.5	5.4	781	2	Q7WRD5	Q7wrds bordetella
1287	65.5	5.4	204	2	Q8LUR35	Q8lur35 oryza sativ	1360	65.5	5.4	811	2	Q593I6	Q593i6 clostridium
1288	65.5	5.4	224	2	Q9ZHI5	Q9zhi5 deaullitoma	1361	65.5	5.4	823	2	Q7MDP5	Q7mdp5 vibrio vuln
1289	65.5	5.4	224	2	Q7TSP2	Q7tsp2 cercopithec	1362	65.5	5.4	823	2	Q8DBE2	Q8dbe2 vibrio vuln
1290	65.5	5.4	236	2	Q7Z3Y4	Q7z3y4 homo sapien	1363	65.5	5.4	836	2	Q6DCD5	Q6dcdd xenopus lae
1291	65.5	5.4	243	2	Q806C8	Q806c8 cercopithec	1364	65.5	5.4	837	1	RA50_MERTH	Q26640 methanobact
1292	65.5	5.4	255	2	Q8B074	Q8b074 mycobacteri	1365	65.5	5.4	856	2	Q86ZJ0	Q86zj0 saccharomyc
1293	65.5	5.4	262	2	Q9RC64	Q9rc64 bacillus ha	1366	65.5	5.4	874	1	PAS1_MOUSE	P87481 mus musculu
1294	65.5	5.4	266	2	Q09514	Q09514 caenorhabdi	1367	65.5	5.4	874	2	Q6PEU2	Q6peu2 mus musculu
1295	65.5	5.4	279	1	PANC_CORGL	Q9x713 cortynobact	1368	65.5	5.4	879	2	Q90ZT8	Q90zt8 gallus gall
1296	65.5	5.4	293	1	Q8RNF4	Q8rfn4 cortynobact	1369	65.5	5.4	892	2	Q8UFU3	Q8ufu3 agrobacteri
1297	65.5	5.4	294	2	Q83GB6	Q83gb6 tropheryma	1370	65.5	5.4	897	2	Q8S6T5	Q8s6t5 oryza sativ
1298	65.5	5.4	294	2	Q83HW2	Q83hw2 tropheryma	1371	65.5	5.4	911	2	Q6R9M2	Q6r9m2 zea mays (m
1299	65.5	5.4	309	2	Q7ZU03	Q7zu03 brachydanto	1372	65.5	5.4	930	2	Q6WDY4	Q6wdy4 giardia lam
1300	65.5	5.4	315	2	Q8FZ49	Q8fz49 leptospira	1373	65.5	5.4	932	2	Q6FHU4	Q6fhu4 candida gla
1301	65.5	5.4	353	2	Q9TOD5	Q9tod5 occurnix co	1374	65.5	5.4	1016	2	Q81X62	Q81x62 homo sapien
1302	65.5	5.4	361	2	Q8WPA2	Q8wpa2 bombxy mori	1375	65.5	5.4	1016	2	Q93H42	Q93h42 streptomyce
1303	65.5	5.4	364	2	Q6WB12	Q6wb12 parachlamyd	1376	65.5	5.4	1096	2	Q94174	Q94174 pneumocysti
1304	65.5	5.4	368	2	Q9A3R5	Q9a3r5 caulobacter	1377	65.5	5.4	1101	2	Q9NXY9	Q9nxy9 homo sapien
1305	65.5	5.4	372	1	SHAK_DROME	P33085 escherichia	1378	65.5	5.4	1125	2	Q7QEC1	Q7qec1 anopheles g
1306	65.5	5.4	375	1	YCDO_ECOLI	P75902 escherichia	1379	65.5	5.4	1150	2	Q96740	Q96740 drosophila
1307	65.5	5.4	375	2	Q8XAS6	Q8xas6 escherichia	1380	65.5	5.4	1157	2	Q7NBS5	Q7nbs5 mycoplasma
1308	65.5	5.4	376	1	CEA2_RAT	Q9jkl5 rattus norv	1381	65.5	5.4	1265	2	Q48870	Q48870 arabisdopsis
1309	65.5	5.4	404	2	Q94F65	Q94f65 oryza sativ	1382	65.5	5.4	1265	2	Q9FTH8	Q9fth8 arabisdopsis
1310	65.5	5.4	404	2	Q7PAR6	Q7far6 oryza sativ	1383	65.5	5.4	1320	2	Q7EZK6	Q7ezk6 oryza sativ
1311	65.5	5.4	409	2	Q28222	Q28222 archaeoglob	1384	65.5	5.4	1359	2	Q6SV64	Q6sv64 cryptococcu
1312	65.5	5.4	420	2	Q6W958	Q6w958 octopus rub	1385	65.5	5.4	1454	2	Q7ZMK4	Q7zmk4 xenopus lae
1313	65.5	5.4	423	2	Q9KFY7	Q9kfy7 bacillus ha	1386	65.5	5.4	1589	2	Q69Z07	Q69z07 mus musculu
1314	65.5	5.4	429	2	Q8LC35	Q8lc35 arabidopsis	1387	65.5	5.4	1625	2	Q637C2	Q637c2 bacillus ce
1315	65.5	5.4	431	2	Q7SY92	Q7sy92 xenopus lae	1388	65.5	5.4	1755	2	Q7XLB6	Q7xlb6 oryza sativ
1316	65.5	5.4	433	1	IHK1_MOUSE	Q6pdl0 mus musculu	1389	65.5	5.4	1781	2	Q6MW15	Q6mw15 oryza sativ
1317	65.5	5.4	435	2	Q9LQ80	Q9lq80 arabidopsis	1390	65.5	5.4	1864	2	Q9BXB2	Q9bxb2 homo sapien
1318	65.5	5.4	437	2	Q8T015	Q8t015 drosophila	1391	65.5	5.4	1864	2	Q9XCD6	Q9xcd6 homo sapien
1319	65.5	5.4	445	1	BPI_RABIT	Q28739 oryctoiaqus	1392	65.5	5.4	1890	2	Q72V39	Q72v39 leptospira
1320	65.5	5.4	448	2	Q9KDR4	Q9kdr4 bacillus ha	1393	65.5	5.4	1984	2	Q9NME7	Q9nme7 viral hemor
1321	65.5	5.4	450	2	Q6T7B6	Q6t7b6 pyrococcus	1394	65.5	5.4	2271	2	Q8SGD5	Q8sgd5 arabidopsis
1322	65.5	5.4	454	2	Q6A097	Q6a097 mus musculu	1395	65.5	5.4	2786	2	Q9VSU2	Q9vsu2 drosophila
1323	65.5	5.4	456	1	E2B_AQUAE	Q67879 aquifex aeo	1396	65.5	5.4	2938	2	Q9SLS2	Q9sls2 arabidopsis
1324	65.5	5.4	458	1	Q84EP4	Q84ep4 wautersia o	1397	65.5	5.4	5457	2	Q83V61	Q83v61 pseudomonas
1325	65.5	5.4	459	1	RSP6_CHLRE	Q01657 chlamydomon	1398	65.5	5.4	13536	2	Q83V60	Q83v60 pseudomonas
1326	65.5	5.4	469	1	YLJ1_CABEL	P34366 caenorhabdi	1399	65.5	5.4	58	2	Q96AL8	Q96al8 homo sapien
1327	65.5	5.4	471	2	Q8BM72	Q8bm72 mus musculu	1400	65.5	5.4	63	2	Q9OZT6	Q9ozt6 rattus norv
1328	65.5	5.4	472	2	Q8VIF7	Q8vif7 rattus norv	1401	65.5	5.4	157	2	Q6B3J8	Q6b3j8 eymphyodon
1329	65.5	5.4	480	2	Q7SL55	Q7sl15 oryza sativ	1402	65.5	5.4	200	2	Q9VPY1	Q9vpy1 drosophila
1330	65.5	5.4	484	2	Q63SF4	Q63sf4 burkholderi	1403	65.5	5.4	221	2	Q8N8Z3	Q8n8z3 homo sapien
1331	65.5	5.4	504	1	OPGC_RALSO	Q8xwc3 raietonia s	1404	65.5	5.4	231	2	Q66104	Q66104 treponema p
1332	65.5	5.4	509	2	Q7YMW1	Q7ymv1 clematis vi	1405	65.5	5.4	244	2	Q6N1N0	Q6n1n0 rhodospseudo
1333	65.5	5.4	520	2	Q7YMW9	Q7ymv9 clematis te	1406	65.5	5.4	245	2	Q8IMU2	Q8im2 drosophila
1334	65.5	5.4	520	2	Q8GHS9	Q8ghs9 clostridium	1407	65.5	5.4	255	2	P95286	P95286 mycobacteri
1335	65.5	5.4	540	2	Q7SBA2	Q7sba2 ashbya gos	1408	65.5	5.4	255	2	Q7TZ97	Q7tz97 mycobacteri
1336	65.5	5.4	542	2	Q59145	Q59145 aeromonas s	1409	65.5	5.4	261	2	Q8XYU8	Q8xyu8 raietonia s
1337	65.5	5.4	546	2	Q6FSU6	Q6fsu6 candida gla	1410	65.5	5.4	264	2	Q6NPM5	Q6npm5 arabidopsis
1338	65.5	5.4	546	2	Q6U103	Q6u1q3 esox reich	1411	65.5	5.4	268	2	Q6CTP2	Q6ctp2 kluyveromyc
1339	65.5	5.4	547	2	Q7S4N2	Q7s4n2 ashbya gos	1412	65.5	5.4	270	2	Q89T01	Q89t01 bradyrhizob
1340	65.5	5.4	562	2	Q05305	Q05305 mycobacteri	1413	65.5	5.4	298	2	Q64PI4	Q64pi4 bacteroides
1341	65.5	5.4	562	2	Q7U0E4	Q7u0e4 mycobacteri	1414	65.5	5.4	302	2	Q858L5	Q858l5 yersinia pe
1342	65.5	5.4	563	2	Q9VST9	Q9vst9 drosophila	1415	65.5	5.4	300	2	Q8SWM6	Q8swm6 drosophila
1343	65.5	5.4	564	2	Q63E34	Q63e34 bacillus ce	1416	65.5	5.4	303	2	Q9PTI9	Q9pti9 neecturus ma
1344	65.5	5.4	575	2	Q8NAG6	Q8nag6 homo sapien	1417	65.5	5.4	305	1	PS11_RAT	Q62632 rattus norv
1345	65.5	5.4	592	2	Q9FKT2	Q9fkt2 arabidopsis	1418	65.5	5.4	310	2	Q935E4	Q935e4 brachydanto

1419	65	5.4	310	2	Q6NSP3	Q6nsp3 brachydanio
1420	65	5.4	318	1	R53_METAC	Q6nru1 methanosaarc
1421	65	5.4	324	2	Q9W4E6	Q9w4e6 dirosophila
1422	65	5.4	329	2	Q8NJI9	Q8nji9 phanerochae
1423	65	5.4	335	2	Q8GK78	Q8gk78 macaca fasc
1424	65	5.4	335	2	Q8CXB5	Q8cxb5 oceanobacil
1425	65	5.4	353	2	Q6LINA4	Q6lina4 photobacter
1426	65	5.4	357	2	Q65WM6	Q65wm6 oryza sativ
1427	65	5.4	359	1	PHOL_ECOLI	P77349 escherichia
1428	65	5.4	360	2	Q6F7M7	Q6f7m7 actinobact
1429	65	5.4	368	2	Q7NW75	Q7nw75 chromobacte
1430	65	5.4	371	2	Q6TNV5	Q6tnv5 brachydanio
1431	65	5.4	372	2	Q7XM21	Q7xm21 oryza sativ
1432	65	5.4	389	2	Q9J302	Q9j302 rice tungro
1433	65	5.4	389	2	Q86367	Q86367 rice tungro
1434	65	5.4	389	2	Q9WQX5	Q9wqx5 rice tungro
1435	65	5.4	389	2	Q9WQX5	Q9wqx5 rice tungro
1436	65	5.4	398	2	Q6F266	Q6f266 bartonella
1437	65	5.4	406	2	Q8KQW8	Q8kqw8 vibrio chol
1438	65	5.4	410	2	Q9XE75	Q9xe75 sorghum bic
1439	65	5.4	413	2	Q9BL66	Q9bl66 caenorhabdi
1440	65	5.4	443	2	Q7SHU7	Q7shu7 neurospora
1441	65	5.4	443	2	Q84YB8	Q84yb8 sorghum bic
1442	65	5.4	443	2	Q8D8W5	Q8d8w5 vibrio vuln
1443	65	5.4	454	2	Q6ZMC8	Q6zmc8 homo sapien
1444	65	5.4	458	1	BPBA_BURCE	P37333 burkholderi
1445	65	5.4	463	2	Q9GSZ4	Q9gsz4 aedes aegypt
1446	65	5.4	473	1	CYPI_CYNCA	P40782 cynara card
1447	65	5.4	474	2	Q8F5U8	Q8f5u8 leptospira
1448	65	5.4	475	1	L1PL_MUSVI	O46647 mustela vis
1449	65	5.4	495	2	Q8LA55	Q8la55 oryza sativ
1450	65	5.4	507	2	Q7JNNE4	Q7jne4 glaucobacter
1451	65	5.4	510	2	Q9LHP8	Q9lhp8 arabidopsis
1452	65	5.4	518	2	Q9Y5X7	Q9y5x7 homo sapien
1453	65	5.4	523	2	Q6ABG6	Q6abg6 caenorhabdi
1454	65	5.4	537	1	OPD2_RALSO	Q8ct53 raietonia s
1455	65	5.4	537	2	Q7BLN9	Q7bln9 lactococcus
1456	65	5.4	537	2	Q9KJN3	Q9kjn3 lactococcus
1457	65	5.4	551	2	Q82T87	Q82t87 nitrosomonas
1458	65	5.4	559	2	Q9AAX4	Q9aax4 caulobacter
1459	65	5.4	573	2	Q8ZQD7	Q8zqd7 salinella
1460	65	5.4	575	2	Q7PWB5	Q7pwb5 anopheles g
1461	65	5.4	577	2	Q69IM9	Q69im9 oryza sativ
1462	65	5.4	590	2	Q8NJI9	Q8nji9 phanerochae
1463	65	5.4	595	2	Q88BP8	Q88bf8 pseudomonas
1464	65	5.4	608	2	Q9Z2A1	Q9z2a1 ratcus norv
1465	65	5.4	614	2	Q9C943	Q9c943 arabidopsis
1466	65	5.4	622	1	PLRL_HUMAN	P16471 homo sapien
1467	65	5.4	627	2	Q7DL53	Q7dl53 arabidopsis
1468	65	5.4	629	1	Q19086	Q19086 caenorhabdi
1469	65	5.4	635	1	SYT_RCCN	Q9dix4 rickettsia
1470	65	5.4	635	2	Q7PB35	Q7pb35 rickettsia
1471	65	5.4	636	2	Q23702	Q23702 arabidopsis
1472	65	5.4	636	2	Q93YQ6	Q93yq6 arabidopsis
1473	65	5.4	638	2	Q948X7	Q948x7 arabidopsis
1474	65	5.4	638	2	Q88AA1	Q88aa1 pseudomonas
1475	65	5.4	641	2	Q03984	Q03984 arabidopsis
1476	65	5.4	662	1	LOXE_MOUSE	P55242 mus musculu
1477	65	5.4	662	1	Q91YW6	Q91yw6 mus musculu
1478	65	5.4	665	2	Q6NXX4	Q6nxx4 homo sapien
1479	65	5.4	672	2	Q9URY1	Q9ury1 schizosacch
1480	65	5.4	672	2	Q9HOK5	Q9hok5 homo sapien
1481	65	5.4	694	2	Q7L3S3	Q7l3s3 homo sapien
1482	65	5.4	697	2	Q6O339	Q6o339 homo sapien
1483	65	5.4	711	1	SYT_HUMAN	P26339 homo sapien
1484	65	5.4	721	2	Q7NV36	Q7nv36 chromobacte
1485	65	5.4	724	2	Q6P4B1	Q6p4b1 homo sapien
1486	65	5.4	725	2	Q6GPI8	Q6gpi8 xenopus lae
1487	65	5.4	726	2	Q9QIJ1	Q9qij1 influenza b
1488	65	5.4	733	2	Q78C28	Q78c28 neurospora
1489	65	5.4	734	2	Q84C34	Q84c34 streptomyce
1490	65	5.4	741	2	Q9P5P3	Q9p5p3 neurospora
1491	65	5.4	744	2	Q6BQP8	Q6bqp8 debaryomyce
1492	65	5.4	747	2	Q7X0I8	Q7x0i8 pseudoalter
1493	65	5.4	760	2	Q6GWS3	Q6gws3 homo sapien
1494	65	5.4	764	2	Q6CWJ4	Q6cwj4 kluyveromyce
1495	65	5.4	773	2	Q9NSW7	Q9nsw7 homo sapien
1496	65	5.4	776	2	Q764N8	Q764n8 geotrichum
1497	65	5.4	787	2	Q75F80	Q75f80 ashbya goss
1498	65	5.4	795	2	Q64Y56	Q64y56 bacteroides
1499	65	5.4	796	2	Q6INB7	Q6inb7 xenopus lae
1500	65	5.4	804	2	Q8TEF5	Q8tef5 homo sapien

ALIGNMENTS

RESULT 1

PPBL_HUMAN STANDARD; PRT: 223 AA.

AC Q96S96; Q8W74; 05-JUN-2004 (Rel. 44, Created)
 DT 05-JUN-2004 (Rel. 44, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE PBP family protein precursor (UNQ1933/PRO4408).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Li N., Wan T., Cao X.,
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA CLARK H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Batton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
 RA Seeshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,
 RA Vanden R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yamaura D.,
 RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.,
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalano D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
 RA Schercher A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 23-37.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;

RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites."
RL Protein Sci. 13:2819-2824(2004).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
CC protein family.

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DR EMBL, AY037148; AAK67629.1; -
DR EMBL, AY559109; AAQ89467.1; -
DR EMBL, BC020779; AAH20779.1; -
DR HSSP, P13696; 1A44.
DR InterPro; IPR001858; PBP.
DR InterPro; IPR008914; PBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
DR PROSITE; PS01220; PBP; 1.
KM Direct protein sequencing; Signal.
FT SIGNAL 1 22
FT CHAIN 23 223 PBP family protein.
FT CONFLICT 125 125 E -> K (in Ref. 2).
FT CONFLICT 211 211 G -> E (in Ref. 1).
FT CONFLICT 220 223 TRRR -> NQARIAC (in Ref. 1).
FT CONFLICT 222 222 R -> Q (in Ref. 2).
SQ SEQUENCE 223 AA; 25431 MW; 9139E4AB8241A4F8 CRC64;

Query Match 99.3%; Score 1196; DB 1; Length 223;
Best Local Similarity 99.1%; Pred. No. 1.6e-106;
Matches 221; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGMTMLVTALLGLMNVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELNIGCKV 60
DB 1 MGMTMLVTALLGLMNVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELNIGCKV 60

QY 61 VPDNNVYQKTSNMEPIYKPGAVDGAITYILVMDPAAPSAERORFWRMVLTIDIKG 120
DB 61 VPDNNVYQKTSNMEPIYKPGAVDGAITYILVMDPAAPSAERORFWRMVLTIDIKG 120

QY 121 ADLKKGKIQGQELSAVQAAPSPAHSGFHRYPFVYLQEGKVISLTPKENTKSGWKMDRF 180
DB 121 ADLKKGKIQGQELSAVQAAPSPAHSGFHRYPFVYLQEGKVISLTPKENTKSGWKMDRF 180
121 ADLKKGKIQGQELSAVQAAPSPAHSGFHRYPFVYLQEGKVISLTPKENTKSGWKMDRF 180
181 INRFHLGEPBASTQFMTOYQDSPTLQAPRGASPEPKTRR 223
DB 181 INRFHLGEPBASTQFMTOYQDSPTLQAPRGASPEPKTRR 223

RESULT 2
PBP_MOUSE STANDARD; PRT; 242 AA.
ID PBP_MOUSE
AC Q9D9G2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE PBP family protein precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,

RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bule C., Hume D.A., Quackenbush J.,
RA Schirni L.M., Kanapin A., Matcoda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi S., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Guerinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Masashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain T., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yangisawa M., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
CC protein family.

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CC EMBL, AK006964; BAB24810.1; -
DR HSSP; P30086; 1BD9.
DR MGD; MGI:1920773; 1700081D17R1k.
DR InterPro; IPR001858; PBP.
DR InterPro; IPR008914; PBP.
DR Pfam; PF01161; PBP; 1.
DR ProDom; PD004330; PBP; 1.
DR PROSITE; PS01220; PBP; 1.
KM Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 242 PBP family protein.
SQ SEQUENCE 242 AA; 26908 MW; 21796A1755FAF01B CRC64;

Query Match 46.6%; Score 561.5; DB 1; Length 242;
Best Local Similarity 46.3%; Pred. No. 1.5e-45;
Matches 113; Conservative 37; Mismatches 67; Indels 27; Gaps 4;

QY 4 TMRLVTAALLGLM-----MVTGDE-DENSP-----CAHEALLDED 39
DB 2 TMRLVTAALLGLMVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFELNIGCKV 61

QY 40 TLPQGLEVFYFELNIGCKVPPDNNVYQKTSNMEPIYKPGAVDGAITYILVMDPA 99
DB 62 VSLCRNLVEFWMEGNISCKTVPCNLYRQCTIPWQAPYVETALLGALLLVMDPDA 121

QY 100 PSRAEPRORFWRMVLTIDIKGADLKKGKIQGQELSAVQAAPSPAHSGFHRYPFVYLQEG 159
DB 122 PSRNPVWKYRHLVSNITGADLKKGKISIRGNVLSDSPPRPETGVHRYQFPVYLQGD 181

QY 160 KVLSLPEKNTKSGWKMDRFNLNRFHLGEPBASTQFMTOYQDSPTLQAPRGASPEPK 219
DB 182 RDLISLVEKANKLGMNLDKFLQGYGLRDPDTSTQFMTOFDE---LSSEGRINDOEQ 238
QY 220 TRRR 223

Db 239 FNOK 242

RESULT 3

Q66KX5 PRELIMINARY; PRT; 202 AA.

AC Q66KX5; 25-OCT-2004 (Tremblrel. 28, Created)

DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE MG85346 protein.

GN Name=MG85346;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Whole;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,

RA Diatchenko L., Marutina K., Farmer A.A., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinchi P., Prange C.,

RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalita D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marz M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Whole;

RA Klein S., Gerhard D.S.,

RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC078524; AAH78524.1; -

DR InterPro; IPR008914; PEBP.

DR Pfam; PF01161; PBP; 1.

DR ProDom; PD004330; PBP; 1.

SQ SEQUENCE 202 AA; 23525 MW; 56AB35C7E76CAF7 CRC64;

Query Match 32.0%; Score 385.5; DB 2; Length 202;

Best local similarity 39.1%; Pred. No. 9.5e-29;

Matches 77; Conservative 43; Mismatches 66; Indels 11; Gaps 6;

QY 12 LLLGLIMVVV---TGDEDENSPCAEHALD-EDTLFC-QGLEVFPELIGNICKVPPDN 65

DB 7 LLLGLISLTARFNTLQAE---CSIRKLFNGEDKFCGKGLDIYSDGLVSCIYIPCF 63

QY 66 NYRQKITN-AMPEPIYKFGAVDGYATYIIWVDPDAPSPAPRPRORFWRWLVTDIKADLK 124

DB 64 DFSWSLSKVMHPLVRYSKAQPGVYKYLIMVDSAPSRWDPKRYWRHMLTLDPGMQLI 123

QY 125 KGL-IGQELSAVQAPSPAPRSGFHRVQFVYLOEGKVISLPPKENTKRGSKMDPLNR 183

DB 124 SGODLTGIDISAHVRPSPPGTGYHRQFVLYEQPIGIVLYLLPEESPRGTWDEAFVER 183

QY 184 FHIGPEASTQFTONTY 200

DB 184 TKLGKPLATQFMAMSH 200

RESULT 4

Q86PT6 PRELIMINARY; PRT; 211 AA.

AC Q86PT6; 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Putative antennal carrier protein A5.

OS Anopheles gambiae (African malaria mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

OX NCBI_TaxID=7165;

RN [1]

RP SEQUENCE FROM N.A.

RC PubMed=14986919;

RX Justice R., Dimitracos S., Walter M.F., Woods D.F., Biesmann H.,

RT "Sexual dimorphic expression of putative antennal carrier protein

RT genes in the malaria vector Anopheles gambiae."

RL Insect Mol. Biol. 12:581-594 (2003).

RN [2]

RP SEQUENCE FROM N.A.

RA Justice R., Dimitracos S., Walter M.F., Woods D.F., Biesmann H.,

RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY187040; AAC039754.1; -

DR HSSP; Q8VINT1; IKN3.

DR InterPro; IPR008914; PEBP.

DR Pfam; PF01161; PBP; 1.

DR ProDom; PD004330; PBP; 1.

SQ SEQUENCE 211 AA; 23141 MW; 79784263A4DAC45E CRC64;

Query Match 21.6%; Score 260.5; DB 2; Length 211;

Best local similarity 33.9%; Pred. No. 1e-16;

Matches 58; Conservative 26; Mismatches 68; Indels 19; Gaps 4;

QY 44 QGLEVFPELIG---NICKGVPPDNVNRKITSWMEPIVFPAGVADGATYILVWVDDAP 100

DB 48 QTKITYPQSDVEVSLGNQLTPQVAKRPLCWEEVP-----SALYTLMDADDPAR 98

QY 101 SRAEPFRFRHMLVTDIKADLKKKIQGQELSAVQAPSPAPRSGFHRVQFVYLOEGK 160

DB 99 SRSNPEKRSKMHVGNIPGADVADGV-----LADYVGSPPPGTGLHRYVFLYKQPSR 154

QY 161 VI---SLPPKENTKRGSKMDPLNRPHLGEPEASTQFTONTYDSPTLQA 208

DB 155 IVFNEVTLSSRNPNRGKMPAEFVKEYLGVPAVGNFYQAQYDDYVELYA 205

RESULT 5

Q7QHW0 PRELIMINARY; PRT; 224 AA.

AC Q7QHW0; 01-MAR-2004 (Tremblrel. 26, Created)

DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE AGCP7981 (Fragment).

GN Name=agC44359; ORFNames=ENSAAG0000014792;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PEST;

RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAAB01008813; EAA04988.1; -
DR HSSP: P30086; 1BD9.
DR InterPro: IPR008914; PEBP.
DR Pfam: PF01161; PBP; 1.
DR ProDom: PD004330; PBP; 1.
DR NON TER 1
FT 1
SQ SEQUENCE 224 AA; 24783 MW; 0C1BC0BA67224D85 CRC64;

Query Match 21.5%; Score 258.5; DB 2; Length 224;
Best Local Similarity 33.9%; Pred. No. 1.7e-16;
Matches 58; Conservative 26; Mismatches 68; Indels 19; Gaps 4;

QY 44 OGLEVFYFELG---NIGCKVVPDCNNYRQKITSWMEPIVKGAVDAGATYILVWVDPAP 100
DB 61 OTIKITTYQSDYEVSLGQULPTTYVKARPKLCWEVP-----SALTILMADPDAP 111
QY 101 SRAEPRORFWRHMLVTDIKGADLKKGKIQQGELSAVQAAPSPAHSGFRYQFFVYLQEGK 160
DB 112 SRSNEMKSWKMWLVGNI PGADVADGV---LADYVSGSPQGTGLHRYVFLVYKQPSR 167
QY 161 VI---SLIPKENTKTSWMDRFLNRFHIGFEPASTQMTQNYQDSPTLQA 208
DB 168 IVFNETVLSSRNPNKNNPAFVVDYELGVPAAGNFYQAQYDVPFLYA 218

RESULT 6

Q7PWN1 PRELIMINARY; PRT; 214 AA.

AC Q7PWN1;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ENSANG00000013993 (Fragment).
GN Name=ENSANG00000011504;
OS Anopheles gambiae str. PEST.
OC Anopheles: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAAB01008984; EAA14862.1; -
DR HSSP: P30086; 1B8H.
DR InterPro: IPR008914; PEBP.
DR Pfam: PF01161; PBP; 1.
DR ProDom: PD004330; PBP; 1.
DR NON TER 1
FT 1
SQ SEQUENCE 214 AA; 23457 MW; A282300BA73605FA CRC64;

Query Match 20.4%; Score 246; DB 2; Length 214;
Best Local Similarity 43.7%; Pred. No. 2.5e-15;
Matches 52; Conservative 13; Mismatches 46; Indels 8; Gaps 2;

QY 84 AVDGAATILVWVDPAPRAEPRORFWRHMLVTDIKGADLKKGKIQQGELSAVQAAPSPA 143
DB 86 ADSGALYTLCTMDPAPSRKERTYEMHMLVGNIPGADV---AQGELISAVVSGSPRQ 141
QY 144 HSGFRYQFFVYLQEGKITSILPKENKT---RGSWKMDRFLNRFHIGFEPASTQMTQ 198
DB 142 GTGLHRYVFLVYKQPSRRLNTSADNRGGFAIRKFAEKYQLGNPVAAGNFYQA 200

RESULT 7

Q7PYP6 PRELIMINARY; PRT; 191 AA.

AC Q7PYP6;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP12373
GN Name=agCG49709; ORFNames=ENSANG00000017428;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxId=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAAB01008987; EAA01113.1; -
DR HSSP: P30086; 1BD9.
DR InterPro: IPR001858; PBP.
DR InterPro: IPR008914; PBP.
DR Pfam: PF01161; PBP; 1.
DR ProDom: PD004330; PBP; 1.
DR ProSite: PS01220; PBP; UNKNOWN_1.
SQ SEQUENCE 191 AA; 21956 MW; 031E661BF29D611D CRC64;

Query Match 19.6%; Score 236; DB 2; Length 191;
Best Local Similarity 36.1%; Pred. No. 2e-14;
Matches 60; Conservative 16; Mismatches 58; Indels 32; Gaps 5;

QY 46 LEVEFP-----ELGNI-----GCKVVPDCNNYRQKITSWMEPIVKGAVDAGATYILVWVDP 96
DB 26 LHVTVPGGLRVNLGNILPTFEVKGVP-----VAMPAPADPAVYALVLTLD 70
QY 97 PDAPSRAPRORFWRHMLVTDIKGADLKKGKIQQGELSAVQAAPSPAHSGFRYQFFVYL 156
DB 71 PDAPSRAPRORFWRHMLVWNI PGMDLAK---GDTLSDYGAAPRKYTGHLHRYVFLYR 126
QY 157 QEGKVI---SLIPKENTKTSWMDRFLNRFHIGFEPASTQMTQ 198
DB 127 QNERIYKESRLSNRSTQGRKPFSTHKFSEKVELGLVAGNFPAQ 172

RESULT 8

PEBP RAT STANDARD; PRT; 166 AA.

AC P31044; P31045;
DT 01-JUL-1993 (Rel. 26, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phosphatidylethanolamine-binding protein (PEBP) (HCNBP) (23 kDa
DE morphine-binding protein) (P23K) [Contains: Hippocampal cholinergic
DE neurostimulating peptide (HCNP)].
GN Name=PBP; Synonyms=PeBP;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=91042640; PubMed=1978248;
RA Grandy D.K., Hanneman E., Bunzow J., Shih M., Machida C.A.,
RA Bidlack J.M., Civelli O.,
RT "Purification, cloning, and tissue distribution of a 23-kDa rat
RT protein isolated by morphine affinity chromatography.";
RL Mol. Endocrinol. 4:1370-1376(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WiStar; TISSUE=Hippocampus;

RX MEDLINE=95364631; PubMed=76375910; DOI=10.1016/0169-328X(95)00029-R;
 RA Tondoh N., Togo S., Agui H., Ojika K.;
 RT "Sequence homology of rat and human HCNP precursor proteins, bovine
 RT phosphatidylethanolamine-binding protein and rat 23-KDa protein
 RT associated with the oploid-binding protein.";
 RL Brain Res. Mol. Brain Res. 30:381-384(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Epididymis, and Liver;
 RX MEDLINE=94311839; PubMed=80376777;
 RA Perry A.C.F., Hall U., Bell A.E., Jones R.;
 RT "Sequence analysis of a mammalian phospholipid-binding protein from
 RT testis and epididymis and its distribution between spermatozoa and
 RT extracellular secretions.";
 RL Biochem. J. 301:235-242(1994).
 RN [4]
 RP SEQUENCE OF 39-55 AND 92-111.
 RC TISSUE=Sperm;
 RX MEDLINE=99031654; PubMed=1932083; DOI=10.1016/0167-4838(91)90114-F;
 RA Jones R., Hall U.;
 RT "A 23 kDa protein from rat sperm plasma membranes shows sequence
 RT similarity and phospholipid binding properties to a bovine brain
 RT cytosolic protein.";
 RL Biochim. Biophys. Acta 1080:78-82(1991).
 RN [5]
 RP SEQUENCE OF 1-11, AND ACETYLTATION.
 RX MEDLINE=92305945; PubMed=1615107;
 RA Ojika K., Kojima S., Ueki Y., Fukushima N., Hayashi K., Yamamoto M.;
 RT "Purification and structural analysis of hippocampal cholinergic
 RT neurostimulating peptide.";
 RL Brain Res. 572:164-171(1992).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=20086088; PubMed=10622376; DOI=10.1016/S0301-0082(99)00021-0;
 RA Ojika K., Mitahe S., Tondoh N., Appel S.H., Otsuka Y., Katada E.,
 RA Matsukawa N.;
 RT "Hippocampal cholinergic neurostimulating peptides (HCNP).";
 RL Prog. Neurobiol. 60:37-83(2000).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE=22478963; PubMed=12591138; DOI=10.1016/S0006-8993(02)04194-X;
 RA Morishita M., Otsuka Y., Matsukawa N., Suzuki H., Nakazawa H.,
 RA Maki M., Katou H., Ueda R., Ojika K.;
 RT "Specific binding of 125I-hippocampal cholinergic neurostimulating
 RT peptide (HCNP) to rat brain membranes: characterization and regional
 RT distribution.";
 RL Brain Res. 965:194-202(2003).
 RL -1- FUNCTION: Binds ATP, opioids and phosphatidylethanolamine. Has
 CC lower affinity for phosphatidylinositol and phosphatidylcholine.
 CC Setine protease inhibitor which inhibits thrombin, neuropsin and
 CC chymotrypsin but not trypsin, tissue type plasminogen activator
 CC and elastase (By similarity).
 CC -1- FUNCTION: HCNP may be involved in the function of the presynaptic
 CC cholinergic neurons of the central nervous system. HCNP increases
 CC the production of choline acetyltransferase but not
 CC acetylcholinesterase. Seems to be mediated by a specific receptor.
 CC -1- SUBUNIT: Has a tendency to form dimers by disulfide cross-linking.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-bound forms exist.
 CC -1- TISSUE SPECIFICITY: Major component of epididymal secretions and
 CC sperm plasma membranes. It is present in cytosols from a variety
 CC of other tissues. Highly expressed in brain.
 CC -1- MISCELLANEOUS: Seems to be associated with memory and learning
 CC disorder.
 CC -1- SIMILARITY: Belongs to the phosphatidylethanolamine-binding
 CC protein family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

CC	EMBL; X75253; CAAS3032.1; -	
DR	EMBL; X75254; CAAS3033.1; -	
DR	EMBL; X71873; CAAS0708.1; -	
DR	PIR; A36126; A36126.	
DR	PIR; S18358; S18358.	
DR	HSSP; P13696; 1B7A.	
DR	Rat-heart-2DPAGE; P31044; -	
DR	RCD; G2017; Pbp.	
DR	InterPro; IPR001858; PBP.	
DR	InterPro; IPR008914; PEBP.	
DR	Pfam; PF01161; PBP; 1.	
DR	ProDom; PD004330; PBP; 1.	
DR	PROSITE; PS01220; PBP; 1.	
KM	Acetylation; ATP-binding; Direct protein sequencing; Lipid-binding; Serine protease inhibitor.	
KW	INIT MET	0
FT	CHAIN	1 186
FT	PERITD	1 11
FT	MOD_RSS	1 1
FT	CONFLICT	48 48
FT	CONFLICT	53 54
SO	SEQUENCE	186 AA; 20670 MW; F2D9DB82C8DD5B5B CRC64;
Qy	Query Match	19.6%; Score 235.5; DB 1; Length 186;
	Best Local Similarity	36.5%; Pred. No. 2.2e-14;
	Matches	57; Conservative 20; Mismatches 60; Indels 19; Gaps 5;
Db	52 ELGNIGKVVPPDCNNYFQKITSMEPIVKCPGAVDGYTLIMVDPDPAFPAERORFWR	111
	35 ELGKVV--LTPQVNNPSSISW-----DGLDPGLTYLTVDPDPAFPRKDPKREWH	84
Qy	112 HMYVTIDKAGDLKKGKIQGQELSAVQAPSPAHSGFRHYGFYVLQSGKVS---- <td>167</td>	167
	85 HFLVNNKNGNDISGGTV---LSRYVSGGPKDGLHRYWLVYEQDPLNCDEPILSNK	140
Db	168 ENKTRGSMKMDRFLNRFPLGPEEASFTQMTQNYQDS	203
	141 SGDNRGKFKYVSPFKKXHYLGAPVAGTGFQAE-WQDS	175
CC	RESULT 9	
CC	PBPB_CABEL	
AC	016264; STANDARD; PRT; 221 AA.	
DT	15-JUL-1999 (Rel. 38, Created)	
DT	15-JUL-1999 (Rel. 38, Last sequence update)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DE	Phosphatidylethanolamine-binding protein homolog F40A3.3.	
GN	ORNames=F40A3.3;	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderinae; Caenorhabditis.	
OX	NCBI_Taxid=6239;	
CC	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Bristol N2;	
RC	MEDLINE=99069613; PubMed=9851916;	
RG	The C. elegans sequencing consortium;	
RG	"Genome sequence of the nematode C. elegans: a platform for	
RT	investigating biology";	
RL	Science 282:2012-2018(1998).	
CC	-1- SIMILARITY: Belongs to the phosphatidylethanolamine-binding	
CC	protein family.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	

SEQ	SEQUENCE	152 AA;	16767 MW;	E3B6C52E3EB3295D	CRC64;
Query Match		19.2%;	Score 231;	DB 1;	Length 152;
Best Local Similarity		37.0%;	Pred. No. 4.6e-14;		
Matches		54;	Conservative 18;	Mismatches 58;	Indels 16; Gaps 5;
QY	55	NIGCKVVP-DCNNRQKITSMEIVKPPGAVDGTITLVMVPDAPSRAPRQRFMRHW	113		
		113			
DB	20	NLGNELPPTQVKNDPTKV-SW-----DAEPALVTLVTPDAPSRKNPFREWHW	70		
		70			
QY	114	LVTIKIGADLKKGIQGOELSAVQAPSPPHSGFHRVQFVYLQEGKVIILLPKENKTRG	173		
		173			
DB	71	LIIISGVNASSGVIV-----LSDIYGSGPPKGTGLHRIYVLVLYKQPGSITP--TQHGKNRP	124		
		124			
QY	174	SWKMDRFLNRFHLSPEASTQFMQTN	199		
		199			
DB	125	NFKVMDFPANKHHLGNPVAAGNPFQAKH	150		
		150			
RESULT 11					
Q6J0U4					
Q6J0U4	PRELIMINARY;	PRT;	179 AA.		
ID					
AC	Q6J0U4;				
DT	05-JUN-2004 (TREMBlrel. 27, Created)				
DT	05-JUN-2004 (TREMBlrel. 27, Last sequence update)				
DT	05-JUN-2004 (TREMBlrel. 27, Last annotation update)				
DE	Phosphatidylethanolamine-binding protein.				
OS	Branchiostoma belcheri tsingtauense.				
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;				
CC	Branchiostoma.				
OX	NCBI_TaxID=155462;				
KN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Zhang S., Li H., Liu Z., Fan C., Xu A.;				
RL	Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AY608669; AAT38121.1; -.				
DR	HSSP; P13696; 1A44.				
DR	InterPro; IPR001858; PBP.				
DR	InterPro; IPR008914; PBP.				
DR	Pfam; PF01161; PBP; 1.				
DR	Prodom; PD004330; PBP; 1.				
DR	PROSITE; PS01220; PBP; 1.				
SQ	SEQUENCE 179 AA; 19814 MW; 3BA62BA3C27029A7 CRC64;				
Query Match		19.2%;	Score 231;	DB 2;	Length 179;
Best Local Similarity		35.6%;	Pred. No. 5.6e-14;		
Matches		58;	Conservative 19;	Mismatches 60;	Indels 26; Gaps 6;
QY	46	LEVFY---PELGNIGCKVVPDCNNRQKITSW-MEPIVKPPGAVDGTITLVMVPDAP	100		
		100			
DB	19	LEVYVGQGVKVDLGN---ELPPTQVKDKPVLVKMDSB-----GAFYTLITLTDADP	66		
		66			
QY	101	SRAPPRQRFMRHWLVTIKIGADLKKGIQGOELSAVQAPSPPHSGFHRVQFVYLQEGK	160		
		160			
DB	67	SRAPPRQRFMRHWLVVNIPIGVDSK---GELISQFVGAGPQGTGLHRIYVLVLYKQPGK	122		
		122			
QY	161	VI-----SILPKENKTRGSMWMDRFLNRFHLSPEASTQFMQTN	198		
		198			
DB	123	ISCENEPKLTNTSGENRQKPSAPDFAKKNVIGAPVAGNLQQAQ	165		
		165			
RESULT 12					
Q6VK60					
Q6VK60	PRELIMINARY;	PRT;	257 AA.		
ID					
AC	Q6VK60; Q8T0L1;				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)				
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)				
DE	CG6180-PA (GH25425p).				
GN	ORFNames=CG6180;				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
CC	Nematoda; Endopterygota; Diptera; Brachycera; Muscomorpha;				

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.H., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jaitai M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon R., Nusekern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Weissman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodgerf, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese B., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weisslock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 RA Kronmiller B., Carlson J.W., Svirskas R.,
 RA Kamlinter J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Friese B., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
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 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Croebly M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hrdceky P., Huang Y., Kamlinter J.S., Millburn G.H., Prochink S.E.,
 RA Smith C.D., Topy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
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 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Friese B., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Munoz J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003637; AA53219.2; -;
 DR EMBL; AF069195; ALJ39340.1; -;
 DR HSSP; P30086; 1BD9.
 DR FLYBASE; FBGN0032453; CG6180.
 DR InterPro; IPR008914; PEBP.
 DR Pfam; PF01161; PBP; 1.
 SQ SEQUENCE 257 AA; 28706 MW; 0CC029521B20D2ED CRC64;
 Query Match 19.0%; Score 229; DB 2; Length 257;
 Best Local Similarity 40.5%; Pred. No. 1,4e-13;
 Matches 53; Conservative 17; Mismatches 51; Indels 10; Gaps 5;
 QY 76 EPIYKFGADGATYLLVWDPDAPSPARPRQFWHMLVTDIKGADLKXGKIQGGLISA 135
 DB 122 EPCYKWE-ANANKLYLTCMTDPAPSRKDPKPEHMLVGNIPGVAGVE---LSA 176
 QY 136 YQAPSPAHSGFRRYQFFVLYOGKVI---SLIPKEN-KTRGSWKMDRFLNRPFLGPEPA 191
 DB 177 YVSGPPPDGLRRYVLYEQRCKLTFDEKRLPNNSGDSGRGKLAEPKRYALGNPIA 236
 QY 192 STQFMONTYOD 202
 DB 237 GNLVQAE-YDD 246
 RESULT 13
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 AC P70296; Q9D869; Q9UJ58;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Phosphatidylethanolamine-binding protein (PEBP) [HGNPp] [Contains:
 DE Hippocampal cholinergic neurostimulating peptide (HCNP)].
 GN Name=Pbp; Synonyms=Pepp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin B., Friesch A.-M.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-11.
 RC STRAIN=BLAB/C; TISSUE=Brain;
 RX MEDLINE=99158500; PubMed=10051191; DOI=10.1016/S0306-4522(98)00215-2;
 RA Matsukawa N., Tooyama I., Kimura H., Yamamoto T., Teugu Y., Oomura Y.,
 RA Ojika K.;
 RT "Increased expression of hippocampal cholinergic neurostimulating
 RT peptide-related components and their messenger RNAs in the hippocampus
 RT of aged senescence-accelerated mice.";

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 CC Onchocercidae; Onchocerca.
 CC NCBI_TaxID=6282;
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 RX MEDLINE=97045813; PubMed=8890735; DOI=10.1016/0378-1119(96)00040-6;
 RA Erttmann K.D., Gallin M.Y.;
 RT "Onchocerca volvulus: Identification of cDNAs encoding a putative
 RT phosphatidyl-ethanolamine-binding protein and a putative partially
 RT processed mRNA precursor";
 RL Gene 174:203-207(1996).
 CC -1: SIMILARITY: Belongs to the phosphatidylethanolamine-binding
 CC protein family.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL, X87989; CAA61242.1; -;
 DR PIR, PC4214; PC4214.
 DR HSP, P13696; IAA4.
 DR InterPro: IPR001858; PBP.
 DR InterPro: IPR008914; PBP.
 DR Pfam, PF01161; PBP; 1.
 DR ProDom, PD004330; PBP; 1.
 DR PROSITE, PS01220; PBP; 1.
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 Db 2 NLGNEILPTQYKQNPVKV-SW-----DAPGKALTLVWTDSDASRKPKVREHHW 52
 QY 114 LVTDIKAGADLKKGKIQGQELSAVQAPSPAHSGFHRVQFPVYLQEGKVISLPPKENTRG 173
 Db 53 LIINISQGVSSGV---LSDYIGSGQPKGTGHRVFLVYKQPGSITD--TQHGGRNP 106
 QY 174 SWKMDRFLNRLGEPKASTQFPTQN 199
 Db 107 NFKVMDPANKKHLGNPVAQNFQAKH 132
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 AC Q9VT08;
 DT 01-MAY-2000 (TREMblrel. 13; Created)
 DT 01-MAY-2000 (TREMblrel. 13; Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 26; Last annotation update)
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 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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 CC Ephydroidea; Drosophilidae; Drosophila.
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 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lesko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Sylvestras R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao O.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zhu S., Zhu X.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs X.H., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
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 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Murry D.M., Nelson C.R.,
 RA Paclebo J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Sylvestras R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs X.H., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Sylvestras R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
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 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.D., Bayraktaroglu L., Berman B.P.,
 RA Bertencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;

RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
 RN [7]
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 RC STRAIN=Bekeley;
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
 RA Cealiker S.;
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
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 DR EMBL; A113352; AAM29357.1; --
 DR HSSP; P13696; 1B7A.
 DR InFect; Q9V108; --
 DR FlyBase; FBgn0037432; CG10298.
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PEBP.
 DR Pfam; PF01161; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
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Search completed: July 20, 2005, 00:07:40
Job time : 231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 00:04:14 ; Search time 155 Seconds
(without alignments)
558.490 Million cell updates/sec

Perfect score: 1204
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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53	1204	100.0	223	14	US-10-223-085-306
59	1204	100.0	223	14	US-10-219-065-232
85	1204	100.0	223	14	US-10-223-084-306
86	1204	100.0	223	14	US-10-223-088-306
87	1204	100.0	223	14	US-10-223-090-306
92	1204	100.0	223	14	US-10-223-087-306
93	1204	100.0	223	14	US-10-223-083-306
96	1204	100.0	223	14	US-10-223-089-306
99	1204	100.0	223	14	US-10-223-081-306
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119	1204	100.0	223	15	US-10-305-654-306

122	1204	100.0	223	15	US-10-081-056-306	Sequence 306, App
127	1204	100.0	223	16	US-10-884-091-61	Sequence 61, App1
128	1200	99.7	223	15	US-10-291-265-245	Sequence 245, App
129	1181	98.1	227	10	US-09-879-401-13	Sequence 3, App1
130	1178	97.8	227	16	US-10-403-142-128	Sequence 128, App
131	1177	97.8	227	11	US-09-978-360A-340	Sequence 540, App
132	1177	97.8	227	17	US-10-926-683-8	Sequence 8, App1
133	1177	97.8	235	15	US-10-403-676-62	Sequence 62, App1
134	1174	97.5	227	16	US-10-403-142-130	Sequence 130, App
135	1173	97.4	227	16	US-10-003-152-2	Sequence 2, App1
136	1173	97.4	227	14	US-10-002-050-2	Sequence 2, App1
137	1173	97.4	227	15	US-10-002-304-2	Sequence 2, App1
138	1173	97.4	227	15	US-10-403-676-58	Sequence 58, App1
139	1173	97.4	235	15	US-10-403-676-60	Sequence 60, App1
140	1171	97.3	227	10	US-09-895-298-107	Sequence 107, App
141	1171	97.3	227	16	US-10-885-039-107	Sequence 107, App
142	1170	97.2	227	16	US-10-403-676-76	Sequence 76, App1
143	1170	97.2	227	15	US-10-403-142-108	Sequence 108, App
144	1167	96.9	227	16	US-10-403-142-126	Sequence 126, App
145	1166	96.8	227	16	US-10-403-142-124	Sequence 124, App
146	1165	96.8	227	16	US-10-403-142-118	Sequence 118, App
147	1163	96.6	227	16	US-10-403-142-110	Sequence 120, App
148	1160	96.3	227	16	US-10-403-142-122	Sequence 122, App
149	1070	88.9	205	15	US-10-403-676-66	Sequence 66, App1
150	1068	88.7	205	15	US-10-403-676-78	Sequence 78, App1
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152	1068	88.7	211	15	US-10-403-676-70	Sequence 70, App1
153	1066	88.5	206	15	US-10-403-676-64	Sequence 64, App1
154	1065	88.5	209	15	US-10-403-142-110	Sequence 110, App
155	1064	88.4	211	15	US-10-403-676-68	Sequence 68, App1
156	1055	87.6	205	16	US-10-403-142-116	Sequence 116, App
157	1055	87.6	209	16	US-10-403-142-112	Sequence 112, App
158	957	79.8	182	15	US-10-403-676-72	Sequence 72, App1
159	957	79.5	182	15	US-10-403-676-74	Sequence 74, App1
160	764	63.5	182	15	US-10-291-265-717	Sequence 717, App
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169	235.5	19.6	187	14	US-10-356-631-105	Sequence 105, App
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171	231	19.2	187	17	US-09-879-401-6	Sequence 6, App1
172	225	18.7	187	17	US-10-362-642B-1	Sequence 1, App1
173	222.5	18.5	187	15	US-10-382-970-4	Sequence 4, App1
174	222.5	18.5	187	16	US-10-384-435B-4	Sequence 4, App1
175	222	18.4	220	15	US-10-382-970-5	Sequence 5, App1
176	222	18.4	220	16	US-10-384-435B-5	Sequence 5, App1
177	218.5	18.1	186	14	US-10-356-631-8	Sequence 8, App1
178	213	17.7	187	15	US-10-382-970-3	Sequence 3, App1
179	213	17.7	187	16	US-10-384-435B-3	Sequence 3, App1
180	211	17.5	187	15	US-10-382-970-2	Sequence 2, App1
181	211	17.5	187	16	US-10-384-435B-2	Sequence 2, App1
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184	205	17.0	187	15	US-10-408-765A-468	Sequence 468, App
185	205	17.0	187	17	US-10-851-921-10	Sequence 10, App1
186	205	17.0	187	17	US-10-362-642B-2	Sequence 2, App1
187	204.5	17.0	176	16	US-10-437-963-169518	Sequence 169518, App
188	204.5	17.0	176	17	US-10-343-477A-30	Sequence 30, App1
189	202.5	16.8	172	17	US-10-343-477A-36	Sequence 36, App1
190	202	16.8	140	16	US-10-408-765A-260	Sequence 260, App
191	195.5	16.2	180	17	US-10-437-963-203900	Sequence 203900, App
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196	193	16.0	180	17	US-10-343-477A-6	Sequence 6, App1
197	192	15.9	180	16	US-10-425-115-193329	Sequence 193329, App
198	192	15.9	180	17	US-10-343-477A-14	Sequence 14, App1

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200	185	15.4	178	16	US-10-437-963-172754	Sequence 172754, Sequence 23651,	273	130	10.7	128	17	US-10-343-477A-22	Sequence 24, Appl1
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202	182	15.1	177	17	US-10-343-477A-18	Sequence 18, Appl1	275	124	10.3	23	16	US-09-895-298-220	Sequence 220, App
203	182	15.1	179	15	US-10-425-114-56802	Sequence 56802, A	276	124	10.3	23	16	US-10-885-039-220	Sequence 220, App
204	182	15.1	179	15	US-10-437-531-2	Sequence 2, Appl1	277	123.5	10.2	219	15	US-10-382-970-8	Sequence 8, Appl1
205	182	15.1	179	15	US-10-437-531-4	Sequence 4, Appl1	278	122.5	10.2	219	15	US-10-382-970-8	Sequence 8, Appl1
206	182	15.1	179	17	US-10-343-477A-62	Sequence 62, Appl1	279	121	10.0	24	16	US-09-895-298-219	Sequence 219, App
207	182	15.1	191	16	US-10-437-963-168356	Sequence 168356, A	280	121	10.0	24	16	US-10-885-039-219	Sequence 219, App
208	180	15.0	177	16	US-10-767-701-33894	Sequence 33894, A	281	120.5	9.9	136	16	US-09-919-178-4	Sequence 4, Appl1
209	179	14.9	177	16	US-10-655-799-26	Sequence 26, Appl1	282	119	9.9	105	17	US-10-343-477A-26	Sequence 26, Appl1
210	177	14.7	181	16	US-10-767-701-51358	Sequence 51358, A	283	113.5	9.4	197	16	US-10-437-963-184618	Sequence 85, Appl1
211	175.5	14.6	174	16	US-10-437-963-160980	Sequence 160980, A	284	110	9.1	112	16	US-10-425-115-254488	Sequence 254488, A
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213	174	14.5	163	16	US-10-425-115-259487	Sequence 259487, A	286	106	8.8	20	16	US-09-895-298-221	Sequence 221, App
214	173	14.4	177	15	US-10-424-599-274975	Sequence 274975, A	287	106	8.8	20	16	US-10-885-039-221	Sequence 8, Appl1
215	173	14.4	185	16	US-10-437-963-148986	Sequence 148986, A	288	105	8.7	106	9	US-09-291-809C-8	Sequence 8, Appl1
216	172	14.3	172	15	US-10-424-599-201099	Sequence 201099, A	289	105	8.7	106	9	US-09-845-849-8	Sequence 8, Appl1
217	169	14.0	173	17	US-10-343-477A-40	Sequence 40, Appl1	290	104.5	8.7	129	15	US-10-425-114-48249	Sequence 48249, A
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223	167.5	13.9	168	16	US-10-767-701-51924	Sequence 51924, A	296	95	7.9	201	16	US-10-432-934-87	Sequence 87, Appl1
224	166	13.8	150	17	US-10-343-477A-2	Sequence 2, Appl1	297	94	7.8	80	16	US-10-425-115-239094	Sequence 239094, A
225	165	13.7	174	17	US-10-343-477A-12	Sequence 12, Appl1	298	92.5	7.7	172	9	US-09-902-331-10	Sequence 10, Appl1
226	164	13.6	175	9	US-09-291-809C-2	Sequence 2, Appl1	299	91.5	7.6	176	16	US-10-425-115-238728	Sequence 6, Appl1
227	164	13.6	175	9	US-09-845-849-2	Sequence 2, Appl1	300	91.5	7.6	176	16	US-10-369-493-930	Sequence 930, App
228	164	13.6	175	10	US-09-919-478-3	Sequence 3, Appl1	301	91.5	7.6	17	16	US-09-895-298-222	Sequence 222, App
229	164	13.6	175	17	US-10-343-477A-61	Sequence 61, Appl1	302	91	7.6	17	16	US-10-885-039-222	Sequence 91, Appl1
230	163	13.5	174	16	US-10-437-963-160617	Sequence 160617, A	303	91	7.6	17	16	US-10-885-039-222	Sequence 91, Appl1
231	161	13.4	180	17	US-10-343-477A-44	Sequence 44, Appl1	304	91	7.6	179	14	US-10-156-761-14011	Sequence 14011, A
232	160	13.3	174	17	US-10-343-477A-60	Sequence 60, Appl1	305	89.5	7.4	176	16	US-09-791-171-50	Sequence 50, Appl1
233	160	13.3	176	15	US-10-424-599-242775	Sequence 242775, A	306	89.5	7.4	176	16	US-09-804-980-50	Sequence 50, Appl1
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235	158.5	13.2	175	16	US-10-425-115-356392	Sequence 356392, A	308	89.5	7.4	196	16	US-10-408-765A-2170	Sequence 2170, App
236	158.5	13.2	176	10	US-09-919-478-41	Sequence 41, Appl1	309	88.5	7.4	174	9	US-09-902-331-8	Sequence 8, Appl1
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239	157.5	13.1	276	16	US-10-491-733-44	Sequence 44, Appl1	312	88	7.3	87	17	US-10-343-477A-34	Sequence 34, Appl1
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243	152.5	12.7	189	15	US-10-425-114-67447	Sequence 67447, A	316	88	7.3	297	11	US-09-885-153-6	Sequence 66, Appl1
244	152	12.6	173	16	US-10-437-963-167316	Sequence 167316, A	317	87.5	7.3	1705	18	US-10-929-3455-37	Sequence 37, Appl1
245	152	12.6	173	17	US-10-343-477A-51	Sequence 51, Appl1	318	87	7.2	89	16	US-10-655-799-27	Sequence 27, Appl1
246	152	12.6	179	15	US-10-262-445-28	Sequence 28, Appl1	319	87	7.2	165	9	US-09-902-331-12	Sequence 12, Appl1
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248	148	12.3	173	16	US-10-425-115-211050	Sequence 211050, A	321	85.5	7.1	490	10	US-09-592-238-7	Sequence 7, Appl1
249	148	12.3	181	14	US-10-356-631-2	Sequence 2, Appl1	322	85.5	7.1	490	16	US-10-712-615-7	Sequence 14, Appl1
250	148	12.3	181	15	US-10-382-970-6	Sequence 6, Appl1	323	85	7.1	165	9	US-09-902-331-14	Sequence 32, Appl1
251	148	12.3	181	16	US-10-384-435B-6	Sequence 6, Appl1	324	83.5	6.9	274	16	US-10-755-889-32	Sequence 32, Appl1
252	147.5	12.3	163	16	US-10-437-963-138695	Sequence 138695, A	325	83.5	6.9	275	9	US-09-925-301-1294	Sequence 113293, A
253	145.5	12.1	193	16	US-10-425-115-358365	Sequence 358365, A	326	83	6.9	232	16	US-10-437-963-112293	Sequence 319, App
254	144.5	12.0	174	16	US-10-425-115-326829	Sequence 326829, A	327	83	6.9	595	15	US-10-170-385-319	Sequence 319, App
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262	137.5	11.4	176	15	US-10-384-435B-7	Sequence 7, Appl1	335	79.5	6.6	595	15	US-10-080-334-247	Sequence 353049, A
263	137.5	11.4	176	16	US-10-384-435B-7	Sequence 7, Appl1	336	79.5	6.6	630	15	US-10-369-493-9044	Sequence 247, App
264	137.5	11.4	177	14	US-10-356-631-5	Sequence 5, Appl1	337	79.5	6.6	648	16	US-10-437-963-193586	Sequence 173586, A
265	137.5	11.4	177	14	US-10-356-631-22	Sequence 22, Appl1	338	79.5	6.6	1042	15	US-10-282-122A-61918	Sequence 61918, A
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271	131.5	10.9	177	14	US-10-356-631-21	Sequence 21, Appl1							

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346	78.5	6.5	285	16	US-10-437-963-153368	Sequence 153368, App	419	73.5	6.1	504	16	US-10-408-765A-18185	Sequence 2185, App
347	78	6.5	191	15	US-10-424-599-285285	Sequence 285285, App	420	73.5	6.1	504	16	US-10-437-963-104780	Sequence 104780, App
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349	77	6.4	579	14	US-10-011-548-2	Sequence 2, App1	422	73.5	6.1	1102	17	US-10-741-600-895	Sequence 895, App
350	77	6.4	1275	14	US-10-128-714-3125	Sequence 3125, App	423	73.5	6.1	1102	17	US-10-741-600-896	Sequence 896, App
351	76.5	6.4	21	16	US-09-895-298-217	Sequence 217, App	424	73.5	6.1	1103	15	US-10-334-143-4	Sequence 4, App1
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353	76.5	6.4	164	15	US-10-424-599-221054	Sequence 221054, App	426	73.5	6.1	1388	15	US-10-408-765A-1139	Sequence 1139, App
354	76.5	6.4	168	9	US-09-902-331-16	Sequence 16, App1	427	73	6.1	1388	15	US-10-369-493-2854	Sequence 2854, App
355	76.5	6.4	1082	16	US-10-437-963-136625	Sequence 136625, App	428	73	6.1	419	15	US-10-424-599-223204	Sequence 223204, App
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357	76	6.3	312	14	US-10-146-772-354	Sequence 354, App	430	73	6.1	419	15	US-10-950-822-2	Sequence 2, App1
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362	76	6.3	436	15	US-10-424-599-242624	Sequence 242624, App	435	73	6.1	1711	18	US-10-023-342A-18	Sequence 38, App1
363	76	6.3	1435	14	US-10-128-714-8125	Sequence 8125, App	436	72.5	6.0	85	15	US-10-424-599-225507	Sequence 225507, App
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365	75.5	6.3	174	15	US-10-424-599-280015	Sequence 280015, App	438	72.5	6.0	158	16	US-10-425-115-304633	Sequence 304633, App
366	75.5	6.3	402	15	US-10-425-115-366759	Sequence 366759, App	439	72.5	6.0	158	16	US-10-425-115-304633	Sequence 304633, App
367	75.5	6.3	404	15	US-10-425-114-67606	Sequence 67606, App	440	72.5	6.0	159	16	US-10-425-115-291948	Sequence 291948, App
368	75.5	6.3	634	16	US-10-437-963-109507	Sequence 109507, App	441	72.5	6.0	321	15	US-10-282-122A-61966	Sequence 61966, App
369	75.5	6.3	816	16	US-10-696-616-44	Sequence 44, App1	442	72.5	6.0	321	15	US-10-424-599-243757	Sequence 243757, App
370	75.5	6.3	965	16	US-10-408-765A-1456	Sequence 1456, App	443	72.5	6.0	321	15	US-10-042-417-58	Sequence 58, App1
371	75.5	6.3	1076	14	US-10-101-235A-6	Sequence 6, App1	444	72.5	6.0	321	15	US-10-679-246-12	Sequence 12, App1
372	75.5	6.3	1101	8	US-08-908-453-12	Sequence 12, App1	445	72.5	6.0	321	15	US-10-652-928-58	Sequence 58, App1
373	75.5	6.3	1101	18	US-10-893-515-74	Sequence 74, App1	446	72.5	6.0	321	15	US-10-264-042-2807	Sequence 2807, App
374	75.5	6.3	1102	16	US-10-408-765A-1342	Sequence 1342, App	447	72.5	6.0	408	15	US-10-264-233-1835	Sequence 1835, App
375	75.5	6.3	1110	14	US-10-101-235A-4	Sequence 4, App1	448	72.5	6.0	721	16	US-10-408-765A-2869	Sequence 2869, App
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377	75	6.2	164	14	US-10-029-386-34205	Sequence 34205, App	450	72.5	6.0	951	16	US-10-425-115-297655	Sequence 297655, App
378	75	6.2	299	18	US-10-724-872A-4326	Sequence 4326, App	451	72.5	6.0	1054	16	US-10-425-115-298655	Sequence 298655, App
379	75	6.2	417	16	US-10-437-963-153712	Sequence 153712, App	452	72.5	6.0	1102	10	US-09-974-573-1	Sequence 1, App1
380	75	6.2	569	15	US-10-369-493-19251	Sequence 19251, App	453	72.5	6.0	1103	13	US-10-071-900-4	Sequence 4, App1
381	75	6.2	980	15	US-10-369-493-1406	Sequence 1406, App	454	72.5	6.0	1211	11	US-09-969-034-4487	Sequence 4487, App
382	75	6.2	980	16	US-10-451-467A-32	Sequence 32, App1	455	72.5	6.0	1211	13	US-10-242-943-14	Sequence 14, App1
383	75	6.2	1041	15	US-10-369-493-1935	Sequence 1935, App	456	72	6.0	210	13	US-10-035-895-2	Sequence 2, App1
384	74.5	6.2	193	16	US-10-767-701-55269	Sequence 55269, App	457	72	6.0	275	15	US-10-282-122A-55720	Sequence 55720, App
385	74.5	6.2	206	15	US-10-424-599-197857	Sequence 197857, App	458	72	6.0	276	18	US-10-504-784-2	Sequence 2, App1
386	74.5	6.2	236	14	US-10-235-175-79	Sequence 79, App1	459	72	6.0	299	9	US-09-808-602-63	Sequence 63, App1
387	74.5	6.2	265	14	US-10-237-386-62	Sequence 62, App1	460	72	6.0	299	14	US-10-800-198-52	Sequence 52, App1
388	74.5	6.2	311	15	US-10-369-493-14114	Sequence 14114, App	461	72	6.0	379	14	US-10-029-386-32938	Sequence 32938, App
389	74.5	6.2	399	15	US-10-369-493-17559	Sequence 17559, App	462	72	6.0	448	15	US-10-425-115-59560	Sequence 59560, App
390	74.5	6.2	455	15	US-10-369-493-5340	Sequence 5340, App	463	72	6.0	643	16	US-10-437-963-187075	Sequence 187075, App
391	74.5	6.2	531	15	US-10-369-493-17970	Sequence 17970, App	464	72	6.0	651	15	US-10-437-963-18865	Sequence 18865, App
392	74.5	6.2	686	16	US-10-011-548-4	Sequence 4, App1	465	72	6.0	803	17	US-10-732-923-9717	Sequence 9717, App
393	74	6.1	233	16	US-10-835-641-25	Sequence 25, App1	466	71.5	5.9	158	16	US-10-425-115-321986	Sequence 321986, App
394	74	6.1	319	15	US-10-282-122A-60415	Sequence 60415, App	467	71.5	5.9	168	16	US-10-425-115-321986	Sequence 321986, App
395	74	6.1	500	16	US-10-739-630-5971	Sequence 5971, App	468	71.5	5.9	194	16	US-10-425-115-346460	Sequence 346460, App
396	74	6.1	504	15	US-10-072-012-863	Sequence 863, App	469	71.5	5.9	203	16	US-10-425-115-304624	Sequence 304624, App
397	74	6.1	548	16	US-10-451-467A-480	Sequence 480, App	470	71.5	5.9	258	15	US-10-425-115-65296	Sequence 65296, App
398	74	6.1	548	16	US-10-451-467A-674	Sequence 674, App	471	71.5	5.9	747	15	US-10-424-599-217157	Sequence 217157, App
399	74	6.1	1061	15	US-10-435-114-53914	Sequence 53914, App	472	71.5	5.9	650	16	US-10-437-963-132976	Sequence 132976, App
400	74	6.1	1061	15	US-10-433-794-18	Sequence 18, App1	473	71.5	5.9	725	15	US-10-732-923-1772	Sequence 1772, App
401	74	6.1	2092	15	US-10-377-035-18	Sequence 18, App1	474	71.5	5.9	725	15	US-10-369-493-2081	Sequence 2081, App
402	74	6.1	2092	15	US-10-042-865-79	Sequence 79, App1	475	71.5	5.9	725	15	US-10-282-122A-65371	Sequence 65371, App
403	74	6.1	2092	16	US-10-408-765A-1967	Sequence 1967, App	476	71.5	5.9	725	15	US-10-282-122A-65746	Sequence 65746, App
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405	74	6.1	2383	18	US-10-499-353A-565	Sequence 565, App	478	71.5	5.9	774	15	US-10-282-122A-42232	Sequence 43232, App
406	74	6.1	2429	15	US-10-288-798-8	Sequence 8, App1	479	71.5	5.9	774	17	US-10-893-671-15	Sequence 15, App1
407	74	6.1	2429	15	US-10-377-035-17	Sequence 17, App1	480	71.5	5.9	1005	15	US-10-369-493-19100	Sequence 19100, App
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412	73.5	6.1	429	15	US-10-072-012-445	Sequence 445, App	485	71	5.9	1498	16	US-10-732-923-85151	Sequence 85151, App
413	73.5	6.1	503	9	US-09-944-807-4	Sequence 4, App1	486	71	5.9	1929	17	US-10-732-923-85151	Sequence 85151, App
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415	73.5	6.1	503	14	US-10-290-198-6	Sequence 6, App1	488	71	5.9	1944	17	US-10-732-923-8814	Sequence 8814, App
416	73.5	6.1	503	15	US-10-072-012-442	Sequence 442, App	489	71	5.9	1944	17	US-10-732-923-8814	Sequence 8814, App
417	73.5	6.1	503	16	US-10-874-015-4	Sequence 4, App1	490	71	5.9	1944	17	US-10-947-476-33	Sequence 33, App1

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522	70	5.8	485	15	US-10-183-687-426	Sequence 426, App	595	69	5.7	773	14	US-10-270-846-35	Sequence 35, Appl
523	70	5.8	503	15	US-10-072-012-120	Sequence 120, App	596	69	5.7	773	14	US-10-734-563-100	Sequence 100, App
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658	68	5.6	475	15	US-10-755-889-100	Sequence 100, App	731	67	5.6	347	9	US-09-950-902-4	Sequence 4, Appl1
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660	68	5.6	475	17	US-10-741-600-1306	Sequence 1306, Ap	733	67	5.6	365	16	US-10-664-421-75	Sequence 75, Appl1
661	68	5.6	475	17	US-10-868-577A-44	Sequence 44, Appl1	734	67	5.6	372	9	US-09-771-161A-203	Sequence 203, Appl1
662	68	5.6	475	17	US-10-868-577A-65	Sequence 65, Appl1	735	67	5.6	372	10	US-09-932-257A-17	Sequence 17, Appl1
663	68	5.6	475	17	US-10-868-549-24	Sequence 24, Appl1	736	67	5.6	372	15	US-10-394-322A-14	Sequence 32, Appl1
664	68	5.6	527	15	US-10-108-260A-3984	Sequence 3984, Ap	737	67	5.6	396	15	US-10-310-154-648	Sequence 648, App
665	68	5.6	585	14	US-10-339-884-1	Sequence 1, Appl1	738	67	5.6	396	15	US-10-374-780A-1781	Sequence 1781, Ap
666	68	5.6	603	16	US-10-788-792-188	Sequence 188, App	739	67	5.6	396	17	US-10-732-923-358	Sequence 358, App
667	68	5.6	629	16	US-10-437-963-174374	Sequence 174374,	740	67	5.6	412	13	US-10-001-054-8	Sequence 8, Appl1
668	68	5.6	634	16	US-10-437-963-190016	Sequence 190016,	741	67	5.6	412	14	US-10-167-749-157	Sequence 157, App
669	68	5.6	848	16	US-10-437-963-118012	Sequence 118012,	742	67	5.6	412	14	US-10-237-535-14	Sequence 14, Appl1
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671	68	5.6	1202	16	US-10-437-963-103812	Sequence 103812,	744	67	5.6	412	14	US-10-323-051-6	Sequence 6, Appl1
672	68	5.6	1523	17	US-10-734-563-94	Sequence 94, Appl1	745	67	5.6	412	15	US-10-170-48A-157	Sequence 157, App
673	68	5.6	1681	15	US-10-037-417-20	Sequence 20, Appl1	746	67	5.6	412	15	US-10-028-157	Sequence 157, App
674	68	5.6	1697	15	US-10-037-417-68	Sequence 68, Appl1	747	67	5.6	412	15	US-10-162-521A-157	Sequence 157, App
675	68	5.6	1723	15	US-10-037-417-18	Sequence 18, Appl1	748	67	5.6	412	16	US-10-755-889-578	Sequence 578, App
676	68	5.6	1841	16	US-10-425-115-360557	Sequence 360557,	749	67	5.6	412	17	US-10-918-851-157	Sequence 157, App
677	68	5.6	1867	15	US-10-466-759-4	Sequence 4, Appl1	750	67	5.6	412	17	US-10-805-667-157	Sequence 157, App
678	68	5.6	1929	15	US-10-210-281-58	Sequence 58, Appl1	751	67	5.6	412	17	US-10-897-359-157	Sequence 157, App
679	68	5.6	19662	15	US-10-084-846A-6	Sequence 6, Appl1	752	67	5.6	412	17	US-10-893-802-157	Sequence 157, App
680	67.5	5.6	128	16	US-10-425-115-216794	Sequence 216794,	753	67	5.6	412	17	US-10-897-360-157	Sequence 157, App
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685	67.5	5.6	164	14	US-10-372-876-664	Sequence 664, App	758	67	5.6	511	16	US-10-437-963-180608	Sequence 180608,
686	67.5	5.6	165	14	US-10-097-065-256	Sequence 256, App	759	67	5.6	543	9	US-09-757-041-2	Sequence 2, Appl1
687	67.5	5.6	165	15	US-10-372-876-256	Sequence 256, App	760	67	5.6	543	15	US-10-004-378A-35	Sequence 35, Appl1
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692	67.5	5.6	299	14	US-10-156-761-11680	Sequence 11680, A	765	67	5.6	567	14	US-10-247-655-103	Sequence 103, App
693	67.5	5.6	309	17	US-10-909-436-50	Sequence 50, Appl1	766	67	5.6	568	8	US-08-813-323A-2	Sequence 2, Appl1
694	67.5	5.6	472	9	US-09-841-758-4	Sequence 4, Appl1	767	67	5.6	568	15	US-10-116-275-173	Sequence 173, App
695	67.5	5.6	497	10	US-09-796-753-116	Sequence 116, App	768	67	5.6	568	15	US-10-004-378A-36	Sequence 36, Appl1
696	67.5	5.6	532	17	US-10-732-923-9798	Sequence 9798, Ap	769	67	5.6	568	17	US-10-042-865-166	Sequence 166, App
697	67.5	5.6	601	15	US-10-051-874-130	Sequence 130, App	770	67	5.6	568	15	US-10-741-600-1358	Sequence 1358, Ap
698	67.5	5.6	609	14	US-10-097-065-237	Sequence 237, App	771	67	5.6	568	17	US-10-741-600-1359	Sequence 1359, Ap
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977	67	5.6	1329	16	US-10-437-963-183534	Sequence 183534, A	1050	66	5.5	524	15	US-10-243-552-861	Sequence 861, App
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981	66.5	5.5	180	15	US-10-223-650-46	Sequence 46, App1	1054	66	5.5	564	15	US-10-424-599-250286	Sequence 250286,
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986	66.5	5.5	233	16	US-10-472-317-26	Sequence 26, App1	1059	66	5.5	680	14	US-10-128-714-8183	Sequence 8183, Ap
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988	66.5	5.5	236	16	US-10-472-317-27	Sequence 27, App1	1061	66	5.5	710	16	US-10-758-846-48	Sequence 84648,
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991	66.5	5.5	310	16	US-10-472-317-12	Sequence 12, App1	1064	66	5.5	738	14	US-10-175-270-2	Sequence 2, App1
992	66.5	5.5	326	16	US-10-437-963-141333	Sequence 141333, A	1065	66	5.5	738	14	US-10-107-857-30	Sequence 30, App1
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995	66.5	5.5	347	17	US-10-883-936-184	Sequence 184, App	1068	66	5.5	743	18	US-10-329-052-34	Sequence 34, App1
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997	66.5	5.5	388	16	US-10-437-963-203686	Sequence 203686, A	1070	66	5.5	746	9	US-09-854-133-185	Sequence 185, App
998	66.5	5.5	404	16	US-10-437-963-102718	Sequence 102718, A	1071	66	5.5	746	14	US-10-144-6498-185	Sequence 185, App
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1006	66.5	5.5	608	14	US-10-156-761-14030	Sequence 14030, A	1079	66	5.5	795	17	US-10-929-150-21	Sequence 21, App1
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1036	66.5	5.5	186	14	US-10-032-2018-60	Sequence 60, App1	1109	66	5.5	1126	14	US-10-309-422-16	Sequence 16, App1
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1121	65.5	5.4	218	15	US-10-333-574-19	Sequence 19, Appl	1194	65.5	5.4	3795	16	US-10-739-930-5776	Sequence 5776, Ap
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1124	65.5	5.4	279	9	US-09-738-626-3632	Sequence 3632, Ap	1197	65.5	5.4	175	15	US-10-425-114-44036	Sequence 44036, A
1125	65.5	5.4	283	15	US-10-424-599-263013	Sequence 263013,	1198	65.5	5.4	180	10	US-09-896-922-44	Sequence 44, Appl
1126	65.5	5.4	288	15	US-10-425-114-46818	Sequence 46818, A	1199	65.5	5.4	180	15	US-10-323-650-44	Sequence 44, Appl
1127	65.5	5.4	315	16	US-10-767-701-41601	Sequence 41601, A	1200	65.5	5.4	185	16	US-10-739-930-6865	Sequence 6865, Ap
1128	65.5	5.4	333	16	US-10-767-701-39689	Sequence 39689, A	1201	65.5	5.4	188	15	US-10-424-599-193127	Sequence 193127,
1129	65.5	5.4	347	15	US-10-424-599-206897	Sequence 206897, A	1202	65.5	5.4	192	16	US-10-437-963-177085	Sequence 177085,
1130	65.5	5.4	371	15	US-10-369-493-9527	Sequence 9527, Ap	1203	65.5	5.4	202	16	US-10-425-115-279123	Sequence 279123,
1131	65.5	5.4	377	15	US-10-425-114-52807	Sequence 52807, A	1204	65.5	5.4	205	16	US-10-437-963-118642	Sequence 118642,
1132	65.5	5.4	379	14	US-10-333-051-4	Sequence 1, Appl1	1205	65.5	5.4	207	16	US-10-739-930-10155	Sequence 10155, A
1133	65.5	5.4	382	14	US-10-333-051-4	Sequence 1, Appl1	1206	65.5	5.4	221	15	US-10-108-260A-3455	Sequence 3455, Ap
1134	65.5	5.4	401	15	US-09-864-694C-1	Sequence 1, Appl1	1207	65.5	5.4	226	15	US-10-424-599-274739	Sequence 274739,
1135	65.5	5.4	404	15	US-10-437-963-150934	Sequence 150934,	1208	65.5	5.4	265	16	US-10-425-115-275862	Sequence 275862,
1136	65.5	5.4	409	15	US-10-369-493-21403	Sequence 21403, A	1209	65.5	5.4	290	16	US-10-370-715B-646	Sequence 646, App
1137	65.5	5.4	409	16	US-10-425-115-299667	Sequence 299667,	1210	65.5	5.4	306	9	US-09-808-602-61	Sequence 61, Appl
1138	65.5	5.4	421	16	US-09-759-1308-76	Sequence 76, Appl	1211	65.5	5.4	306	10	US-09-800-198-50	Sequence 50, Appl1
1139	65.5	5.4	421	16	US-10-741-790-76	Sequence 76, Appl	1212	65.5	5.4	336	15	US-10-369-493-10669	Sequence 10669, A
1140	65.5	5.4	427	14	US-10-179-784-3	Sequence 3, Appl1	1213	65.5	5.4	363	16	US-10-425-115-320414	Sequence 320414,
1141	65.5	5.4	435	16	US-10-408-765A-929	Sequence 929, Appl	1214	65.5	5.4	406	16	US-10-451-467A-548	Sequence 548, App
1142	65.5	5.4	442	10	US-09-895-298-139	Sequence 139, App	1215	65.5	5.4	421	17	US-10-732-923-2710	Sequence 2710, Ap
1143	65.5	5.4	442	16	US-10-885-039-139	Sequence 139, App	1216	65.5	5.4	449	14	US-10-277-032-2	Sequence 2, Appl1
1144	65.5	5.4	467	16	US-10-425-115-200145	Sequence 200145,	1217	65.5	5.4	449	15	US-10-681-223-2	Sequence 2, Appl1
1145	65.5	5.4	472	16	US-10-787-421-2	Sequence 2, Appl1	1218	65.5	5.4	454	15	US-10-380-873B-3	Sequence 3, Appl1
1146	65.5	5.4	480	16	US-10-437-963-202594	Sequence 202594,	1219	65.5	5.4	459	11	US-09-950-822-11	Sequence 11, Appl
1147	65.5	5.4	487	17	US-10-813-588-2	Sequence 2, Appl1	1220	65.5	5.4	503	15	US-10-282-122A-59917	Sequence 59917, A
1148	65.5	5.4	513	16	US-10-437-963-150933	Sequence 150933,	1221	65.5	5.4	510	15	US-10-369-493-3993	Sequence 3993, Ap
1149	65.5	5.4	524	15	US-10-108-260A-3442	Sequence 3442, Ap	1222	65.5	5.4	518	16	US-10-723-860-2039	Sequence 2039, Ap
1150	65.5	5.4	539	15	US-10-295-027-1299	Sequence 1299, Ap	1223	65.5	5.4	530	16	US-10-112-944-284	Sequence 284, App
1151	65.5	5.4	539	16	US-10-783-528-81	Sequence 81, Appl	1224	65.5	5.4	555	15	US-10-424-599-228544	Sequence 228544,
1152	65.5	5.4	539	16	US-10-783-528-82	Sequence 82, Appl	1225	65.5	5.4	564	15	US-10-424-599-272057	Sequence 272057,
1153	65.5	5.4	539	17	US-10-813-588-6	Sequence 6, Appl1	1226	65.5	5.4	579	16	US-10-437-963-118857	Sequence 118857,
1154	65.5	5.4	547	16	US-10-425-115-281483	Sequence 281483,	1227	65.5	5.4	597	15	US-10-287-971-74	Sequence 74, Appl1
1155	65.5	5.4	550	16	US-10-425-115-257869	Sequence 257869,	1228	65.5	5.4	622	14	US-10-177-293-373	Sequence 373, App
1156	65.5	5.4	555	15	US-10-104-047-1176	Sequence 3176, Ap	1229	65.5	5.4	622	15	US-10-295-027-112	Sequence 112, App
1157	65.5	5.4	586	15	US-10-295-027-1300	Sequence 1300, Ap	1230	65.5	5.4	622	15	US-10-295-027-744	Sequence 744, App
1158	65.5	5.4	586	17	US-10-813-588-4	Sequence 4, Appl1	1231	65.5	5.4	622	15	US-10-058-270A-40	Sequence 40, Appl
1159	65.5	5.4	592	15	US-10-425-114-58893	Sequence 58893, A	1232	65.5	5.4	629	15	US-10-344-741-23	Sequence 23, Appl
1160	65.5	5.4	593	17	US-10-732-923-22811	Sequence 22811, A	1233	65.5	5.4	636	16	US-10-425-115-289578	Sequence 289578,
1161	65.5	5.4	593	16	US-10-425-115-267109	Sequence 267109,	1234	65.5	5.4	652	16	US-10-437-963-135557	Sequence 135557,
1162	65.5	5.4	610	16	US-10-437-963-161701	Sequence 161701,	1235	65.5	5.4	674	14	US-10-425-114-65041	Sequence 65041, A
1163	65.5	5.4	611	16	US-10-437-963-173002	Sequence 173002,	1236	65.5	5.4	674	14	US-10-173-123-9	Sequence 9, Appl1
1164	65.5	5.4	641	15	US-10-312-352-11	Sequence 11, Appl	1237	65.5	5.4	674	15	US-10-451-822-1	Sequence 1, Appl
1165	65.5	5.4	643	15	US-10-282-122A-67033	Sequence 67033, A	1238	65.5	5.4	674	15	US-10-451-822-41	Sequence 41, Appl
1166	65.5	5.4	646	16	US-10-437-963-107426	Sequence 107426,	1239	65.5	5.4	674	15	US-10-451-822-43	Sequence 43, Appl
1167	65.5	5.4	664	17	US-10-732-923-8234	Sequence 8234, Ap	1240	65.5	5.4	681	14	US-10-173-123-7	Sequence 7, Appl1
1168	65.5	5.4	664	15	US-10-389-647-469	Sequence 469, App	1241	65.5	5.4	681	15	US-10-332-447-19	Sequence 19, Appl
1169	65.5	5.4	681	16	US-09-759-1308-75	Sequence 75, Appl	1242	65.5	5.4	700	16	US-10-408-765A-2425	Sequence 2425, Ap
1170	65.5	5.4	681	16	US-10-741-790-75	Sequence 75, Appl	1243	65.5	5.4	721	15	US-10-424-599-172399	Sequence 172399,
1171	65.5	5.4	715	10	US-09-759-1308-73	Sequence 73, Appl	1244	65.5	5.4	738	14	US-10-173-123-13	Sequence 13, Appl
1172	65.5	5.4	715	13	US-10-003-132-2	Sequence 2, Appl1	1245	65.5	5.4	745	9	US-10-173-123-11	Sequence 11, Appl
1173	65.5	5.4	715	16	US-10-741-790-73	Sequence 73, Appl1	1246	65.5	5.4	773	14	US-09-808-602-60	Sequence 60, Appl
1174	65.5	5.4	815	16	US-10-425-115-231544	Sequence 231544,	1247	65.5	5.4	773	9	US-09-800-198-49	Sequence 49, Appl
1175	65.5	5.4	932	16	US-10-381-906-200	Sequence 200, App	1248	65.5	5.4	777	9	US-09-925-301-1115	Sequence 115, Ap
1176	65.5	5.4	983	16	US-10-425-115-297852	Sequence 297852,	1249	65.5	5.4	780	15	US-10-425-114-47924	Sequence 47924, A
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1178	65.5	5.4	1016	14	US-10-156-761-10696	Sequence 10696, A	1251	65.5	5.4	820	15	US-10-425-114-53704	Sequence 53704, A
1179	65.5	5.4	1027	16	US-10-425-115-300455	Sequence 300455,	1252	65.5	5.4	820	15	US-10-425-114-70197	Sequence 70197, A
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1181	65.5	5.4	1039	16	US-10-425-115-299558	Sequence 299558,	1254	65.5	5.4	848	15	US-10-332-426-3	Sequence 3, Appl1
1182	65.5	5.4	1101	14	US-10-177-293-106	Sequence 106, App	1255	65.5	5.4	848	15	US-10-380-873B-1	Sequence 1, Appl1
1183	65.5	5.4	1101	16	US-10-408-765A-2181	Sequence 2181, App	1256	65.5	5.4	850	9	US-09-808-602-88	Sequence 58, Appl
1184	65.5	5.4	1101	16	US-10-723-860-3158	Sequence 3158, Ap	1257	65.5	5.4	850	10	US-09-800-198-47	Sequence 47, Appl
1185	65.5	5.4	1359	16	US-10-437-963-190032	Sequence 190032,	1258	65.5	5.4	877	9	US-09-391-340-8	Sequence 8, Appl1
1186	65.5	5.4	1360	16	US-10-473-574-112	Sequence 12, Appl	1259	65.5	5.4	877	9	US-09-948-369-8	Sequence 16, Appl1
1187	65.5	5.4	1379	16	US-10-437-963-113781	Sequence 113781,	1260	65.5	5.4	921	17	US-10-257-021-16	Sequence 9, Appl1
1188	65.5	5.4	1378	16	US-10-437-963-183595	Sequence 183595,	1261	65.5	5.4	931	17	US-10-616-689-9	Sequence 8, Appl1
1189	65.5	5.4	1737	9	US-10-437-963-194264	Sequence 194264,	1262	65.5	5.4	951	14	US-10-379-616-8	Sequence 8, Appl1
1190	65.5	5.4	1864	14	US-09-832-292-27	Sequence 27, Appl	1263	65.5	5.4	951	16	US-10-473-127-354	Sequence 354, App
1191	65.5	5.4	1864	14	US-10-153-244-9	Sequence 9, Appl1	1264	65.5	5.4	952	15	US-10-616-624-8	Sequence 8, Appl1
1192	65.5	5.4	1864	16	US-10-343-903-23	Sequence 23, Appl	1265	65.5	5.4	952	17	US-10-616-689-2	Sequence 2, Appl1

1266	65	5.4	983	9	US-09-808-602-73	Sequence 73, Appl	1339	64.5	5.4	387	15	US-10-424-599-213199	Sequence 212199, A
1267	65	5.4	983	14	US-10-013-136-2	Sequence 2, Appl1	1340	64.5	5.4	395	15	US-10-425-114-71141	Sequence 71141, A
1268	65	5.4	1100	15	US-10-369-493-13176	Sequence 13176, A	1341	64.5	5.4	437	18	US-10-724-972A-5345	Sequence 5345, Ap
1269	65	5.4	1153	16	US-10-367-094-116	Sequence 116, App	1342	64.5	5.4	461	15	US-10-424-599-205993	Sequence 205993,
1270	65	5.4	1261	15	US-10-012-697-1483	Sequence 1483, Ap	1343	64.5	5.4	475	16	US-10-425-115-324876	Sequence 324876,
1271	65	5.4	1296	14	US-10-302-279-60	Sequence 60, Appl	1344	64.5	5.4	501	9	US-09-931-087A-3	Sequence 3, Appl1
1272	65	5.4	1396	16	US-10-437-963-136020	Sequence 136020,	1345	64.5	5.4	501	14	US-10-062-923-3	Sequence 3, Appl1
1273	65	5.4	1396	16	US-10-437-963-136020	Sequence 136020,	1346	64.5	5.4	502	16	US-10-381-906-183	Sequence 183, App
1274	65	5.4	1416	17	US-10-732-923-1695	Sequence 1695, Ap	1347	64.5	5.4	508	15	US-10-104-047-3488	Sequence 3488, Ap
1275	65	5.4	1444	16	US-10-437-963-128076	Sequence 128076,	1348	64.5	5.4	538	16	US-10-425-115-301341	Sequence 301341,
1276	65	5.4	1412	16	US-10-473-127-351	Sequence 351, App	1349	64.5	5.4	548	17	US-10-732-923-20699	Sequence 20699, A
1277	65	5.4	1412	16	US-10-473-127-352	Sequence 352, App	1350	64.5	5.4	549	16	US-10-425-115-281520	Sequence 281520,
1278	65	5.4	1412	16	US-10-473-127-356	Sequence 356, App	1351	64.5	5.4	549	16	US-10-425-115-281525	Sequence 281525,
1279	65	5.4	1412	16	US-10-473-127-357	Sequence 357, App	1352	64.5	5.4	549	17	US-10-732-923-20887	Sequence 20887, A
1280	65	5.4	1415	16	US-10-408-765A-2282	Sequence 2282, Ap	1353	64.5	5.4	550	14	US-10-411-253-4	Sequence 4, Appl1
1281	65	5.4	1417	16	US-10-473-127-348	Sequence 348, App	1354	64.5	5.4	553	17	US-10-732-923-3128	Sequence 3128, Ap
1282	65	5.4	1420	14	US-10-473-127-359	Sequence 359, App	1355	64.5	5.4	560	9	US-09-841-132-492	Sequence 492, App
1283	65	5.4	1420	16	US-10-379-616-4	Sequence 4, Appl1	1356	64.5	5.4	560	16	US-10-972-155-492	Sequence 492, App
1284	65	5.4	1420	16	US-10-473-127-349	Sequence 349, App	1357	64.5	5.4	573	15	US-10-325-066A-684	Sequence 684, App
1285	65	5.4	1420	16	US-10-473-127-358	Sequence 358, App	1358	64.5	5.4	573	15	US-10-374-780A-2784	Sequence 2784, App
1286	65	5.4	1424	15	US-10-418-027-1	Sequence 358, App	1359	64.5	5.4	612	15	US-10-282-122A-65672	Sequence 65672, A
1287	65	5.4	1424	15	US-10-473-127-347	Sequence 1, Appl1	1360	64.5	5.4	613	16	US-10-451-467A-278	Sequence 278, App
1288	65	5.4	1424	16	US-10-473-127-350	Sequence 347, App	1361	64.5	5.4	615	16	US-10-381-906-193	Sequence 193, App
1289	65	5.4	1424	16	US-10-473-127-350	Sequence 350, App	1362	64.5	5.4	617	15	US-10-282-122A-43178	Sequence 43178, A
1290	65	5.4	1424	16	US-10-473-127-360	Sequence 360, App	1363	64.5	5.4	623	16	US-10-437-963-143769	Sequence 143769,
1291	65	5.4	1434	10	US-09-754-032-10	Sequence 10, Appl	1364	64.5	5.4	643	17	US-10-732-923-20897	Sequence 20897, A
1292	65	5.4	1434	14	US-10-421-446-10	Sequence 10, Appl	1365	64.5	5.4	658	17	US-10-732-923-14988	Sequence 14988, A
1293	65	5.4	1438	16	US-10-333-894A-19	Sequence 19, Appl	1366	64.5	5.4	664	17	US-10-949-437-43	Sequence 43, Appl
1294	65	5.4	1438	16	US-08-954-701A-19	Sequence 19, Appl	1367	64.5	5.4	664	17	US-10-915-366-4	Sequence 4, Appl1
1295	65	5.4	1447	9	US-09-898-533-5	Sequence 5, Appl1	1368	64.5	5.4	771	16	US-10-437-963-170390	Sequence 170390,
1296	65	5.4	1447	10	US-09-754-032-19	Sequence 19, Appl	1369	64.5	5.4	812	16	US-10-437-963-162597	Sequence 162597,
1297	65	5.4	1447	10	US-10-421-446-19	Sequence 19, Appl	1370	64.5	5.4	817	16	US-10-437-963-155863	Sequence 155863,
1298	65	5.4	1447	18	US-10-791-844-6	Sequence 19, Appl	1371	64.5	5.4	921	16	US-10-437-963-189826	Sequence 189826,
1299	65	5.4	1447	18	US-10-437-963-138317	Sequence 6, Appl1	1372	64.5	5.4	932	16	US-10-715-632-20	Sequence 20, Appl
1300	65	5.4	1522	16	US-10-473-127-355	Sequence 183317,	1373	64.5	5.4	953	16	US-10-437-963-126195	Sequence 126195,
1301	65	5.4	1522	16	US-10-473-127-355	Sequence 355, App	1374	64.5	5.4	1002	15	US-10-437-963-126195	Sequence 1, Appl1
1302	65	5.4	1398	16	US-10-437-963-194719	Sequence 199992,	1375	64.5	5.4	1011	16	US-10-154-086-1	Sequence 1, Appl1
1303	65	5.4	1398	16	US-10-437-963-194719	Sequence 194719,	1376	64.5	5.4	1014	14	US-10-411-253-3	Sequence 189808,
1304	65	5.4	1494	16	US-10-437-963-157544	Sequence 157544,	1377	64.5	5.4	1037	15	US-10-154-086-15	Sequence 3, Appl1
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1306	64.5	5.4	87	17	US-10-424-599-152739	Sequence 28, Appl	1379	64.5	5.4	1074	15	US-10-369-493-359	Sequence 359, App
1307	64.5	5.4	118	15	US-10-343-477A-28	Sequence 45198, A	1380	64.5	5.4	1078	16	US-10-425-115-299769	Sequence 299769,
1308	64.5	5.4	128	14	US-10-156-136-44	Sequence 44, Appl	1381	64.5	5.4	1127	16	US-10-425-115-299769	Sequence 124142,
1309	64.5	5.4	128	15	US-10-051-874-153	Sequence 153, App	1382	64.5	5.4	1127	16	US-10-437-963-124142	Sequence 102965,
1310	64.5	5.4	128	15	US-10-051-874-154	Sequence 154, App	1383	64.5	5.4	1173	16	US-10-616-082-95	Sequence 95, Appl
1311	64.5	5.4	128	15	US-10-188-832-151	Sequence 151, App	1384	64.5	5.4	1311	16	US-10-437-963-183648	Sequence 183648,
1312	64.5	5.4	128	16	US-10-809-654-20	Sequence 20, Appl	1385	64.5	5.4	1473	16	US-10-437-963-192876	Sequence 192876,
1313	64.5	5.4	128	16	US-10-809-655-20	Sequence 20, Appl	1386	64.5	5.4	1601	16	US-10-437-963-183647	Sequence 183647,
1314	64.5	5.4	166	16	US-10-425-115-255625	Sequence 255625,	1387	64.5	5.4	1689	16	US-10-425-115-300648	Sequence 300648,
1315	64.5	5.4	175	9	US-09-738-626-6309	Sequence 6309, Ap	1388	64.5	5.4	1777	16	US-10-425-115-300643	Sequence 300643,
1316	64.5	5.4	178	15	US-10-282-122A-59107	Sequence 59107, A	1389	64.5	5.4	1815	15	US-10-085-198-10	Sequence 10, Appl
1317	64.5	5.4	202	16	US-10-472-317-29	Sequence 29, Appl	1390	64.5	5.4	1856	15	US-10-085-198-8	Sequence 8, Appl1
1318	64.5	5.4	212	17	US-10-822-613-33	Sequence 33, Appl	1391	64.5	5.4	4025	16	US-10-437-963-193926	Sequence 193926,
1319	64.5	5.4	213	17	US-10-849-615-67	Sequence 67, Appl	1392	64.5	5.4	55	16	US-10-437-963-143208	Sequence 143208,
1320	64.5	5.4	213	18	US-10-728-723-198	Sequence 198, App	1393	64	5.3	150	15	US-10-424-599-163864	Sequence 163864,
1321	64.5	5.4	228	16	US-10-437-963-181730	Sequence 181730,	1394	64	5.3	150	17	US-10-732-923-21250	Sequence 21950, A
1322	64.5	5.4	239	9	US-09-965-528-20	Sequence 20, Appl	1395	64	5.3	150	17	US-10-732-923-21250	Sequence 21950, A
1323	64.5	5.4	239	11	US-09-969-984-20	Sequence 20, Appl	1396	64	5.3	170	16	US-10-437-963-175187	Sequence 175187,
1324	64.5	5.4	253	15	US-10-282-122A-54672	Sequence 54672, A	1397	64	5.3	180	10	US-09-896-923-36	Sequence 36, Appl
1325	64.5	5.4	263	11	US-09-979-948C-1	Sequence 1, Appl1	1398	64	5.3	180	10	US-09-896-923-37	Sequence 37, Appl
1326	64.5	5.4	278	15	US-10-187-975-120	Sequence 120, App	1399	64	5.3	180	10	US-09-896-923-38	Sequence 38, Appl
1327	64.5	5.4	290	15	US-10-187-975-48	Sequence 48, Appl	1400	64	5.3	180	10	US-09-896-923-39	Sequence 39, Appl
1328	64.5	5.4	299	15	US-10-282-122A-55576	Sequence 55576, A	1401	64	5.3	180	10	US-09-896-923-41	Sequence 41, Appl
1329	64.5	5.4	300	14	US-10-270-875-45	Sequence 45, Appl	1402	64	5.3	180	10	US-09-896-923-42	Sequence 42, Appl
1330	64.5	5.4	300	14	US-10-270-878-45	Sequence 45, Appl	1403	64	5.3	180	10	US-09-896-923-43	Sequence 43, Appl
1331	64.5	5.4	300	14	US-10-270-710-45	Sequence 45, Appl	1404	64	5.3	180	10	US-09-896-923-45	Sequence 45, Appl
1332	64.5	5.4	300	14	US-10-270-859-45	Sequence 45, Appl	1405	64	5.3	180	10	US-09-896-923-47	Sequence 47, Appl
1333	64.5	5.4	300	14	US-10-270-859-45	Sequence 45, Appl	1406	64	5.3	180	10	US-09-896-923-48	Sequence 48, Appl
1334	64.5	5.4	300	14	US-10-270-846-45	Sequence 45, Appl	1407	64	5.3	180	15	US-10-223-650-35	Sequence 35, Appl
1335	64.5	5.4	322	16	US-10-856-499-784	Sequence 784, App	1408	64	5.3	180	15	US-10-223-650-36	Sequence 36, Appl
1336	64.5	5.4	354	15	US-10-099-332-58	Sequence 58, Appl	1409	64	5.3	180	15	US-10-223-650-37	Sequence 37, Appl
1337	64.5	5.4	354	15	US-10-044-564-58	Sequence 58, Appl	1410	64	5.3	180	15	US-10-223-650-38	Sequence 38, Appl
1338	64.5	5.4	358	16	US-10-381-906-187	Sequence 187, App	1411	64	5.3	180	15	US-10-223-650-39	Sequence 39, Appl

1412	64	5.3	180	15	US-10-223-650-41	Sequence 41, Appl
1413	64	5.3	180	15	US-10-223-650-42	Sequence 42, Appl
1414	64	5.3	180	15	US-10-223-650-43	Sequence 43, Appl
1415	64	5.3	180	15	US-10-223-650-45	Sequence 45, Appl
1416	64	5.3	180	15	US-10-223-650-47	Sequence 47, Appl
1417	64	5.3	180	15	US-10-223-650-48	Sequence 48, Appl
1418	64	5.3	197	15	US-10-335-977-9521	Sequence 9521, Ap
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1422	64	5.3	214	9	US-09-811-384-11	Sequence 11, Appl
1423	64	5.3	214	15	US-10-404-286-11	Sequence 11, Appl
1424	64	5.3	214	16	US-10-762-967-2	Sequence 2, Appl
1425	64	5.3	216	15	US-10-630-932-3	Sequence 3, Appl
1426	64	5.3	220	16	US-10-767-701-43898	Sequence 43858, A
1427	64	5.3	222	16	US-10-693-629-666	Sequence 66, Appl
1428	64	5.3	235	16	US-10-437-963-166870	Sequence 166870,
1429	64	5.3	237	9	US-09-940-166A-6	Sequence 6, Appl
1430	64	5.3	237	14	US-10-227-694-1	Sequence 1, Appl
1431	64	5.3	237	16	US-10-762-967-6	Sequence 6, Appl
1432	64	5.3	237	17	US-10-754-212-2	Sequence 2, Appl
1433	64	5.3	247	10	US-09-823-187-81	Sequence 81, Appl
1434	64	5.3	247	15	US-10-466-164-69	Sequence 69, Appl
1435	64	5.3	255	16	US-10-437-963-134382	Sequence 134382,
1436	64	5.3	272	16	US-10-437-963-196318	Sequence 196318,
1437	64	5.3	285	14	US-10-156-761-7886	Sequence 7886, Ap
1438	64	5.3	287	16	US-10-437-963-155765	Sequence 155765,
1439	64	5.3	288	15	US-10-282-122A-70759	Sequence 70759, A
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1442	64	5.3	316	15	US-10-424-599-216682	Sequence 216682,
1443	64	5.3	320	15	US-10-425-114-43318	Sequence 43318, A
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1445	64	5.3	330	14	US-10-128-714-8134	Sequence 8134, Ap
1446	64	5.3	344	15	US-10-424-599-224120	Sequence 224120,
1447	64	5.3	354	15	US-10-282-122A-47673	Sequence 47673, A
1448	64	5.3	357	15	US-10-369-493-4272	Sequence 4272, Ap
1449	64	5.3	360	11	US-09-833-245-1807	Sequence 1807, Ap
1450	64	5.3	363	16	US-10-425-115-330768	Sequence 330768,
1451	64	5.3	379	16	US-10-425-115-342069	Sequence 342069,
1452	64	5.3	397	15	US-10-282-122A-54779	Sequence 54779, A
1453	64	5.3	404	15	US-10-282-122A-72698	Sequence 72698, A
1454	64	5.3	414	17	US-10-738-634A-3	Sequence 3, Appl
1455	64	5.3	415	15	US-10-425-114-55218	Sequence 55218, A
1456	64	5.3	421	15	US-10-289-762-535	Sequence 535, App
1457	64	5.3	442	15	US-10-282-122A-47144	Sequence 47144, A
1458	64	5.3	445	16	US-10-437-963-119135	Sequence 119135,
1459	64	5.3	449	15	US-10-289-762-1114	Sequence 1114, Ap
1460	64	5.3	456	16	US-10-437-963-118704	Sequence 118704,
1461	64	5.3	477	15	US-10-425-114-65173	Sequence 65173, A
1462	64	5.3	503	9	US-09-815-242-13854	Sequence 13854, A
1463	64	5.3	503	15	US-10-282-122A-76200	Sequence 76200, A
1464	64	5.3	512	9	US-09-764-868-654	Sequence 654, App
1465	64	5.3	512	9	US-09-764-868-1080	Sequence 1080, Ap
1466	64	5.3	512	16	US-10-679-620-70	Sequence 70, Appl
1467	64	5.3	517	16	US-10-679-620-68	Sequence 68, Appl
1468	64	5.3	519	16	US-10-679-620-66	Sequence 66, Appl
1469	64	5.3	529	14	US-10-156-761-8846	Sequence 8846, Ap
1470	64	5.3	552	15	US-10-369-493-4108	Sequence 4108, Ap
1471	64	5.3	560	16	US-10-425-115-274008	Sequence 274008,
1472	64	5.3	568	16	US-10-437-963-202324	Sequence 202324,
1473	64	5.3	612	9	US-09-815-242-11295	Sequence 11295, A
1474	64	5.3	612	9	US-09-895-913A-262	Sequence 262, App
1475	64	5.3	612	15	US-10-282-122A-58626	Sequence 58626, A
1476	64	5.3	634	15	US-10-369-493-13304	Sequence 13304, A
1477	64	5.3	658	16	US-10-425-115-332796	Sequence 332796,
1478	64	5.3	664	15	US-10-369-493-18321	Sequence 18321, A
1479	64	5.3	728	17	US-10-661-398-29	Sequence 29, Appl
1480	64	5.3	755	16	US-10-437-963-203661	Sequence 203661,
1481	64	5.3	776	10	US-09-836-923-2	Sequence 2, Appl
1482	64	5.3	776	10	US-10-435-766-1	Sequence 1, Appl
1483	64	5.3	776	15	US-10-223-650-2	Sequence 2, Appl
1484	64	5.3	776	15	US-10-280-962-45	Sequence 45, Appl

Search completed: July 20, 2005, 00:21:56
Job time : 173 secs

1485	64	5.3	776	15	US-10-280-962-46	Sequence 46, Appl
1486	64	5.3	776	15	US-10-408-601-32	Sequence 32, Appl
1487	64	5.3	776	15	US-10-298-680-45	Sequence 45, Appl
1488	64	5.3	776	15	US-10-298-680-46	Sequence 46, Appl
1489	64	5.3	776	16	US-10-702-400-55	Sequence 55, Appl
1490	64	5.3	776	16	US-10-702-400-56	Sequence 56, Appl
1491	64	5.3	776	17	US-10-805-650-55	Sequence 55, Appl
1492	64	5.3	776	17	US-10-805-650-56	Sequence 56, Appl
1493	64	5.3	776	17	US-10-734-563-32	Sequence 32, Appl
1494	64	5.3	776	17	US-10-734-563-90	Sequence 90, Appl
1495	64	5.3	776	18	US-10-853-973A-1	Sequence 1, Appl
1496	64	5.3	870	16	US-10-437-963-202330	Sequence 202330,
1497	64	5.3	886	14	US-10-017-161-2068	Sequence 2068, Ap
1498	64	5.3	904	16	US-10-408-765A-1999	Sequence 1999, Ap
1499	64	5.3	984	15	US-10-149-310-118	Sequence 118, App
1500	64	5.3	992	15	US-10-138-588-22	Sequence 22, Appl

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: July 19, 2005, 23:59:53 ; Search time 168 Seconds
(without alignments)

513.378 Million cell updates/sec

US-10-036-214-61

Title:

1204

Sequence: 1 MGWTRLVTAALTLGLMMVV.....PTLQAPRGASBPQKTROR 223

Scoring table:

BLOSUM62

GAPOP 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

A_Geneseq_16dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

RESULT 1

ID AAB18923 standard; protein; 223 AA.

DE A novel polypeptide designated PRO4408.

PN WO200056889-A2.

PD 28-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 3; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 2

ID AAU83707 standard; protein; 223 AA.

DE Human PRO protein, Seq ID No 232.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 5; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 3

ID ABB84969 standard; protein; 223 AA.

DE Human PRO4408 protein sequence SEQ ID NO:306.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 5; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 4

ID ABB95575 standard; protein; 223 AA.

DE Human angiogenesis related protein PRO4408 SEQ ID NO: 306.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLMAN K J.

PA (MARK) MASTERS S A.

PA (PANU) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

Query Match

Best Local Similarity 100.0%; Score 1204; DB 5; Length 223;

RESULT 5

ID ABU69117 standard; protein; 223 AA.

DE Human PRO polypeptide #15.

PN US2003032061-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 6

ID ABU80854 standard; protein; 223 AA.

DE Human PRO polypeptide #16.

PN US2003036635-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 7

ID AB033820 standard; protein; 223 AA.

DE Novel human secreted and transmembrane protein PRO4408.

PN US2003045687-A1.

PD 06-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 8

ID AB019433 standard; protein; 223 AA.

DE Human secreted / transmembrane polypeptide PRO4408.

PN US2003027249-A1.

PD 06-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 9

ID ABU69094 standard; protein; 223 AA.

DE Human PRO polypeptide #15.

PN US2003008348-A1.

PD 09-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 10

ID ABU82163 standard; protein; 223 AA.

DE Novel human secreted and transmembrane protein PRO4408.

PN US2003088063-A1.

PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 11

ID ABU81558 standard; protein; 223 AA.

DE Human secreted polypeptide PRO4408.

PN US2002192751-A1.

PD 19-DEC-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 12

ID ADA76586 standard; protein; 223 AA.

DE Novel human secreted and transmembrane protein PRO4408.

PN US2003036114-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 6; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;

RESULT 13

ID ABJ72343 standard; protein; 223 AA.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 14
ID ABR72471 standard; protein; 223 AA.
DE Human PRO4408 protein.
FN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 15
ID ABO34366 standard; protein; 223 AA.
DE Human secreted/transmembrane polypeptide PRO 4405.
FN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 16
ID ABO25141 standard; protein; 223 AA.
DE Human secreted/transmembrane protein PRO4408.
FN US2003044842-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 17
ID ABR72173 standard; protein; 223 AA.
DE Human membrane bound receptor/protein PRO4408 amino acid sequence.
FN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 18
ID ADB83722 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 19
ID ADB80828 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 20
ID ADB73369 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 21
ID ADB78451 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 22
ID ADB85099 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
FN US2003073817-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 23
ID ADB78205 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 24
ID ADB87271 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
FN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 25
ID ADB84853 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
FN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 26
ID ADB83968 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 27
ID ADB73123 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
FN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 28
ID AAB39111 standard; protein; 223 AA.
DE Human PRO4408 protein.
FN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 29
ID AAB39048 standard; protein; 223 AA.
DE Human PRO4408 protein.
FN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 30
ID ADC36961 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
FN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 31
ID ADC21951 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
FN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 32
ID ADC29917 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003092063-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 33
ID ADC49982 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 34
ID ADC49181 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 35
ID ADC49698 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 36
ID ADC47559 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 37
ID ADC47304 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 38
ID ADC78179 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 39
ID ADD06414 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 40
ID ADD0595 standard; protein; 223 AA.
DE Human secreted/transmembrane PRO polypeptide #153.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;

Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 41
ID ADC77933 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 42
ID ADD1555 standard; protein; 223 AA.
DE Human secreted/transmembrane PRO polypeptide #153.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 43
ID ADD50896 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 44
ID ADD51142 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 45
ID ADD37348 standard; protein; 223 AA.
DE Human secreted/transmembrane PRO polypeptide #153.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 46
ID ADD50623 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 47
ID ADD50377 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 48
ID ADD51388 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 7; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 49
ID ADC48935 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;

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RESULT 50
ID ADE21106 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 51
ID ADE05950 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 52
ID ADD75179 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 53
ID ADD75925 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 54
ID ADD85157 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 55
ID ADD86983 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 56
ID ADE20860 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 57
ID ADE39157 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 58
ID ADE05704 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 59
ID ADD76171 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 60
ID ADD78529 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 61
ID ADD41556 standard; protein; 223 AA.
DE Human secreted/transmembrane PRO polypeptide #153.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 62
ID ADE21352 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 63
ID ADD7467 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 64
ID ADE20614 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 65
ID ADD5679 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 66
ID ADD74195 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 67
ID ADD74441 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 68
ID ADD76171 standard; protein; 223 AA.
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DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 69
ID ADD85663 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 70
ID ADE05212 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 71
ID ADD75425 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 72
ID ADD76969 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 73
ID ADD86737 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 74
ID ADD78205 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 75
ID ADD77713 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 76
ID ADD77959 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 77
ID ADB65417 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 78
ID ADD73949 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 79
ID ADD74687 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 80
ID ADD77215 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 81
ID ADB65909 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 82
ID ADE05458 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 83
ID ADD74933 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 84
ID ADR09260 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003134327-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 85
ID ADE05745 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 86
ID ADE27299 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003096962-A1.

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PD 22-MAY-2003
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 87
ID ADG11362 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 88
ID ADG12141 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 89
ID ADP94698 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 90
ID ADG06794 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 91
ID ADH39138 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 92
ID ADH43739 standard; protein; 223 AA.
DE Human PRO polypeptide #153.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 93
ID ADG34228 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 94
ID ADI33698 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 95
ID ADH6392 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 96
ID ADI29953 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 97
ID ADM7350 standard; protein; 223 AA.
DE Novel human secreted and transmembrane protein PRO4408.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 98
ID ADK3084 standard; protein; 223 AA.
DE Human PRO polypeptide #153.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 99
ID ADK6708 standard; protein; 223 AA.
DE Human PRO polypeptide #116.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1204; DB 8; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-128;
RESULT 100
ID AAV14138 standard; protein; 223 AA.
DE Human novel protein #9.
PN WO200155457-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 99.7%; Score 1200; DB 4; Length 223;
Best Local Similarity 99.6%; Pred. No. 2.2e-127;
RESULT 101
ID ADI34902 standard; protein; 223 AA.
DE Cardiovascular disorder plasma polypeptide (CPP) 11 precursor sequence.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 99.3%; Score 1196; DB 8; Length 223;
Best Local Similarity 99.1%; Pred. No. 6.2e-127;
RESULT 102
ID AAY94263 standard; protein; 227 AA.
DE Human phospholipid binding protein 2, PLBP2.
PN US6063767-A.
PD 16-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 98.1%; Score 1181; DB 3; Length 227;
Best Local Similarity 98.6%; Pred. No. 3.2e-125;
RESULT 103
ID ADB8899 standard; protein; 227 AA.
DE Human Phospholipid binding protein, PLBP2.
PN US2003119730-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 98.1%; Score 1181; DB 7; Length 227;
Best Local Similarity 98.6%; Pred. No. 3.2e-125;
RESULT 104
ID ADK70502 standard; protein; 227 AA.
DE Respiratory disease differentially expressed protein #68.
PN WO2003010283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
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Query Match 98.1%; Score 1181; DB 8; Length 227;
 Best Local Similarity 98.6%; Pred. No. 3.2e-125;
 RESULT 105
 ID ADK68202 standard; protein; 227 AA.
 DE Novel NOVX protein #64.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 97.8%; Score 1178; DB 7; Length 227;
 Best Local Similarity 98.6%; Pred. No. 7.1e-125;
 RESULT 106
 ID ADR49191 standard; protein; 227 AA.
 DE Human NOV8 protein.
 PN US2004162336-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASM/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LIL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLET I.
 PA (PATR/) PATTURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOV S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 97.8%; Score 1178; DB 8; Length 227;
 Best Local Similarity 98.6%; Pred. No. 7.1e-125;
 RESULT 107
 ID AAY35976 standard; protein; 227 AA.
 DE Extended human secreted protein sequence, SEQ ID NO. 225.
 PN WO9931236-A2.
 PD 24-JUN-1999.
 PA (GEST) GENSET.
 Query Match 97.8%; Score 1177; DB 2; Length 227;
 Best Local Similarity 98.6%; Pred. No. 9.2e-125;
 RESULT 108
 ID AAY64647 standard; protein; 227 AA.
 DE Human phosphatidylethanolamine-binding protein.
 PN WO953051-A2.
 PD 21-OCT-1999.
 PA (GEST) GENSET.
 Query Match 97.8%; Score 1177; DB 3; Length 227;
 Best Local Similarity 98.6%; Pred. No. 9.2e-125;
 RESULT 109
 ID AAG00016 standard; protein; 227 AA.
 DE Human secreted protein #4.
 PN EPI033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 97.8%; Score 1177; DB 3; Length 227;
 Best Local Similarity 98.6%; Pred. No. 9.2e-125;
 RESULT 110
 ID AAB8590 standard; protein; 227 AA.
 DE Human hydrophobic domain containing protein clone HP03880 #94.

PN WO200112660-A2.
 PD 22-FEB-2001.
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 Query Match 97.8%; Score 1177; DB 4; Length 227;
 Best Local Similarity 98.6%; Pred. No. 9.2e-125;
 RESULT 111
 ID ADP19284 standard; protein; 227 AA.
 DE Human secreted polypeptide #135.
 PN US2004110939-A1.
 PD 10-JUN-2004.
 PA (GEST) GENSET SA.
 Query Match 97.8%; Score 1177; DB 8; Length 227;
 Best Local Similarity 98.6%; Pred. No. 9.2e-125;
 RESULT 112
 ID ADG76149 standard; protein; 235 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 62).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 97.8%; Score 1177; DB 7; Length 235;
 Best Local Similarity 98.6%; Pred. No. 9.6e-125;
 RESULT 113
 ID ADK68204 standard; protein; 227 AA.
 DE Novel NOVX protein #65.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 97.5%; Score 1174; DB 7; Length 227;
 Best Local Similarity 98.2%; Pred. No. 2e-124;
 RESULT 114
 ID ADR49193 standard; protein; 227 AA.
 DE Human NOV81 protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASM/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LIL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLET I.
 PA (PATR/) PATTURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOV S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 97.5%; Score 1174; DB 8; Length 227;
 Best Local Similarity 98.2%; Pred. No. 2e-124;
 RESULT 115
 ID AAB48368 standard; protein; 227 AA.
 DE Human SCL protein sequence (clone ID 345452).
 PN WO200078802-A2.
 PD 28-DEC-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 97.4%; Score 1173; DB 4; Length 227;

Best local Similarity 98.2%; Pred. No. 2.6e-124;
RESULT 116
ID ADG76145 standard; protein; 227 AA.
DE Human NOVX protein to treat human pathological conditions (Segid 58).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.4%; Score 1173; DB 7; Length 227;
Best local Similarity 98.2%; Pred. No. 2.6e-124;
RESULT 117
ID ADI34900 standard; protein; 227 AA.
DE Cardiovascular disorder plasma polypeptide (CPE) 10 precursor sequence.
PN WO2004005931-A1.
PD 15-JUN-2004.
PA (GENE-) GENEPROT INC.
Query Match 97.4%; Score 1173; DB 8; Length 227;
Best local Similarity 98.2%; Pred. No. 2.6e-124;
RESULT 118
ID ADG76147 standard; protein; 235 AA.
DE Human NOVX protein to treat human pathological conditions (Segid 60).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.4%; Score 1173; DB 7; Length 235;
Best local Similarity 98.2%; Pred. No. 2.7e-124;
RESULT 119
ID AAB24482 standard; protein; 227 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:107.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.3%; Score 1171; DB 3; Length 227;
Best local Similarity 98.2%; Pred. No. 4.4e-124;
RESULT 120
ID ADG76163 standard; protein; 227 AA.
DE Human NOVX protein to treat human pathological conditions (Segid 76).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.2%; Score 1170; DB 7; Length 227;
Best local Similarity 98.2%; Pred. No. 5.7e-124;
RESULT 121
ID ADK68182 standard; protein; 227 AA.
DE Novel NOVX protein #54.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.2%; Score 1170; DB 7; Length 227;
Best local Similarity 98.2%; Pred. No. 5.7e-124;
RESULT 122
ID ADR49171 standard; protein; 227 AA.
DE Human NOV8a protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO-) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER I.

PA (PAT/) PATTRAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 97.2%; Score 1170; DB 8; Length 227;
Best local Similarity 98.2%; Pred. No. 5.7e-124;
RESULT 123
ID AAB3330 standard; protein; 227 AA.
DE Human ORFX ORF3094 polypeptide sequence SEQ ID NO:6188.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 97.0%; Score 1168; DB 3; Length 227;
Best local Similarity 98.2%; Pred. No. 9.7e-124;
RESULT 124
ID ADK68200 standard; protein; 227 AA.
DE Novel NOVX protein #63.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 96.9%; Score 1167; DB 7; Length 227;
Best local Similarity 97.7%; Pred. No. 1.3e-123;
RESULT 125
ID ADR49189 standard; protein; 227 AA.
DE Human NOV8j protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER I.
PA (PAT/) PATTRAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 96.9%; Score 1167; DB 8; Length 227;
Best local Similarity 97.7%; Pred. No. 1.3e-123;
RESULT 126
ID ADK68198 standard; protein; 227 AA.
DE Novel NOVX protein #62.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 96.8%; Score 1166; DB 7; Length 227;
Best local Similarity 97.7%; Pred. No. 1.6e-123;
RESULT 127

ID ADR49187 standard; protein; 227 AA.
 DE Human NOV61 protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASW/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLET I.
 PA (PATY/) PATTURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 96.8%; Score 1166; DB 8; Length 227;
 Best Local Similarity 97.7%; Pred. No. 1.6e-123;
 RESULT 128
 ID ADR68192 standard; protein; 227 AA.
 DE Novel NOVX protein #59.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 96.8%; Score 1165; DB 7; Length 227;
 Best Local Similarity 97.7%; Pred. No. 2.1e-123;
 RESULT 129
 ID ADR49181 standard; protein; 227 AA.
 DE Human NOV6f protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASW/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLET I.
 PA (PATY/) PATTURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.

PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 96.8%; Score 1165; DB 8; Length 227;
 Best Local Similarity 97.7%; Pred. No. 2.1e-123;
 RESULT 130
 ID ADR68194 standard; protein; 227 AA.
 DE Novel NOVX protein #60.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 96.6%; Score 1163; DB 7; Length 227;
 Best Local Similarity 97.7%; Pred. No. 3.6e-123;
 RESULT 131
 ID ADR49183 standard; protein; 227 AA.
 DE Human NOV6g protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASW/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILT/) MILLET I.
 PA (PATY/) PATTURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMIT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match 96.6%; Score 1163; DB 8; Length 227;
 Best Local Similarity 97.7%; Pred. No. 3.6e-123;
 RESULT 132
 ID ADR68196 standard; protein; 227 AA.
 DE Novel NOVX protein #61.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 96.3%; Score 1160; DB 7; Length 227;
 Best Local Similarity 97.7%; Pred. No. 7.8e-123;
 RESULT 133
 ID ADR49185 standard; protein; 227 AA.
 DE Human NOV6h protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASW/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.

PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLET I.
 PA (PAT/) PATURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match
 Best Local Similarity 96.3%; Score 1160; DB 8; Length 227;
 RESULT 134
 ID AD134903 standard; protein; 201 AA.
 DE Cardiovascular disorder plasma polypeptide (CPP) 11 mature protein.
 PN WO2004005931-A1.
 PD 15-JAN-2004.
 PA (GENE-) GENEPROT INC.
 Query Match
 Best Local Similarity 90.3%; Score 1087; DB 8; Length 201;
 RESULT 135
 ID ADG76153 standard; protein; 206 AA.
 DE Human NOVX protein to treat human pathological conditions (Segid 66).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.9%; Score 1070; DB 7; Length 206;
 RESULT 136
 ID ADG76165 standard; protein; 205 AA.
 DE Human NOVX protein to treat human pathological conditions (Segid 78).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 98.5%; Score 1068; DB 7; Length 205;
 RESULT 137
 ID ADK68188 standard; protein; 209 AA.
 DE Novel NOVX protein #57.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.7%; Score 1068; DB 7; Length 209;
 RESULT 138
 ID ADK49177 standard; protein; 209 AA.
 DE Human NOV8d protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.
 PA (CASW/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (EILE/) EILERMAN K.
 PA (FERV/) FERRANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLEY D.

PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALY/) MALYANKAR U M.
 PA (MILL/) MILLET I.
 PA (PAT/) PATURAJAN M.
 PA (PEYM/) PEYMAN J A.
 PA (RAST/) RASTELLI L.
 PA (RIEG/) RIEGER D.
 PA (SHEN/) SHENOY S.
 PA (SHIM/) SHIMKETS R.
 PA (SMT/) SMITHSON G.
 PA (STON/) STONE D.
 PA (VERN/) VERNET C.
 PA (VOSS/) VOSS E.
 Query Match
 Best Local Similarity 88.7%; Score 1068; DB 8; Length 209;
 RESULT 139
 ID ADG76157 standard; protein; 211 AA.
 DE Human NOVX protein to treat human pathological conditions (Segid 70).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.7%; Score 1068; DB 7; Length 211;
 RESULT 140
 ID ADG76151 standard; protein; 206 AA.
 DE Human NOVX protein to treat human pathological conditions (Segid 64).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.5%; Score 1066; DB 7; Length 206;
 RESULT 141
 ID ADK68184 standard; protein; 209 AA.
 DE Novel NOVX protein #55.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.0%; Score 1065; DB 7; Length 209;
 RESULT 142
 ID AD134901 standard; protein; 205 AA.
 DE Cardiovascular disorder plasma polypeptide (CPP) 10 mature protein.
 PN WO2004005931-A1.
 PD 15-JAN-2004.
 PA (GENE-) GENEPROT INC.
 Query Match
 Best Local Similarity 88.4%; Score 1064; DB 8; Length 205;
 RESULT 143
 ID ADG76155 standard; protein; 211 AA.
 DE Human NOVX protein to treat human pathological conditions (Segid 68).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 88.4%; Score 1064; DB 7; Length 211;
 RESULT 144
 ID ADK68190 standard; protein; 205 AA.
 DE Novel NOVX protein #58.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 87.6%; Score 1055; DB 7; Length 205;
 RESULT 145
 ID ADK49179 standard; protein; 205 AA.
 DE Human NOV8e protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDOG F.
 PA (BURG/) BURGESS C.

PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILT/) MILLET I.
PA (PATR/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match
Best Local Similarity 87.6%; Score 1055; DB 8; Length 205;
RESULT 146
ID ADK68186 standard; protein; 209 AA.
DE Novel NOVX protein #56.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 97.0%; Pred. No. 6e-111;
RESULT 147
ID ADR49175 standard; protein; 209 AA.
DE Human NOV8c protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILT/) MILLET I.
PA (PATR/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match
Best Local Similarity 87.6%; Score 1055; DB 8; Length 209;
RESULT 148
ID ADR49173 standard; protein; 210 AA.

DE Human NOV8b protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILT/) MILLET I.
PA (PATR/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match
Best Local Similarity 87.6%; Score 1054.5; DB 8; Length 210;
RESULT 149
ID ADG76159 standard; protein; 182 AA.
DE Human NOVX protein to treat human pathological conditions (Segid 72).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 79.8%; Score 961; DB 7; Length 182;
RESULT 150
ID ADG76161 standard; protein; 182 AA.
DE Human NOVX protein to treat human pathological conditions (Segid 74).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 79.5%; Score 957; DB 7; Length 182;
RESULT 151
ID AUI14374 standard; protein; 182 AA.
DE Human novel protein #245.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSSEQ INC.
Query Match
Best Local Similarity 63.2%; Score 761; DB 4; Length 182;
RESULT 152
ID ADH80692 standard; protein; 183 AA.
DE Human polypeptide #9.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LITU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (OIAN/) OIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.

PA (DRMA/) DRMANAC R T.
Query Match 61.8%; Score 743.5; DB 8; Length 183;
Best Local Similarity 81.2%; Pred. No. 1.2e-75;
RESULT 153
ID AAB24591 standard; protein; 149 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:217.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 57.1%; Score 688; DB 3; Length 149;
Best Local Similarity 97.7%; Pred. No. 1.9e-69;
RESULT 154
ID AAY11860 standard; protein; 121 AA.
DE Human 5' EST secreted protein SEQ ID No: 460.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GSEST-) GENSEST.
Query Match 54.2%; Score 652; DB 2; Length 121;
Best Local Similarity 99.2%; Pred. No. 1.7e-65;
RESULT 155
ID ADI34940 standard; protein; 242 AA.
DE Mouse CYP orthologue sequence.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 46.6%; Score 561.5; DB 8; Length 242;
Best Local Similarity 46.3%; Pred. No. 8.6e-55;
RESULT 156
ID AAB24597 standard; protein; 86 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:223.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.7%; Score 394; DB 3; Length 86;
Best Local Similarity 93.7%; Pred. No. 2.2e-36;
RESULT 157
ID AAB24487 standard; protein; 87 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:112.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.7%; Score 394; DB 3; Length 87;
Best Local Similarity 93.7%; Pred. No. 2.3e-36;
RESULT 158
ID AAR27897 standard; protein; 187 AA.
DE HCNP protein.
PN EP511816-A2.
PD 04-NOV-1992.
PA (SUMU-) SUMITOMO PHARM CO LTD.
PA (OUIK/) OUIKA K.
PA (YAMA/) YAMAMOTO M.
Query Match 19.6%; Score 235.5; DB 2; Length 187;
Best Local Similarity 36.5%; Pred. No. 6.6e-18;
RESULT 159
ID AAR49942 standard; protein; 187 AA.
DE Rat hippocampal cholinergic neurotrophic peptide precursor.
PN WO9405788-A1.
PD 17-MAR-1994.
PA (SUMU-) SUMITOMO PHARM CO LTD.
PA (YAMA/) YAMAMOTO M.
Query Match 19.6%; Score 235.5; DB 2; Length 187;
Best Local Similarity 36.5%; Pred. No. 6.6e-18;
RESULT 160
ID ADF30544 standard; protein; 187 AA.
DE Rat angiogenesis modulating protein #58.
PN US2003162706-A1.
PD 28-AUG-2003.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 19.6%; Score 235.5; DB 7; Length 187;
Best Local Similarity 36.5%; Pred. No. 6.6e-18;
RESULT 161
ID ADF30542 standard; protein; 187 AA.
DE Rat angiogenesis modulating protein #57.

PN US2003162706-A1.
PD 28-AUG-2003.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 19.6%; Score 235.5; DB 7; Length 187;
Best Local Similarity 36.5%; Pred. No. 6.6e-18;
RESULT 162
ID AAE37272 standard; protein; 105 AA.
DE Human gene 1 encoded secreted protein HNM1K76, SEQ ID NO:35.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 19.3%; Score 232; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
RESULT 163
ID AAY94265 standard; protein; 152 AA.
DE Onchocerca volvulus phosphatidylethanolamine binding protein D1.
PN US6063767-A.
PD 16-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 19.2%; Score 231; DB 3; Length 152;
Best Local Similarity 37.0%; Pred. No. 1.6e-17;
RESULT 164
ID ADH89002 standard; protein; 152 AA.
DE Onchocerca volvulus phosphatidylethanolamine binding protein, PE-BP.
PN US2003119730-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 19.2%; Score 231; DB 7; Length 152;
Best Local Similarity 37.0%; Pred. No. 1.6e-17;
RESULT 165
ID ABB62148 standard; protein; 178 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 13236.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 19.0%; Score 229; DB 4; Length 178;
Best Local Similarity 40.5%; Pred. No. 3.4e-17;
RESULT 166
ID AAE21676 standard; protein; 187 AA.
DE Mouse phosphoethanolamine binding protein (PEBP).
PN WO200218623-A2.
PD 07-MAR-2002.
PA (NOVS-) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
Query Match 18.7%; Score 225; DB 5; Length 187;
Best Local Similarity 35.1%; Pred. No. 1e-16;
RESULT 167
ID ABB64993 standard; protein; 187 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21771.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 18.5%; Score 222.5; DB 4; Length 187;
Best Local Similarity 38.6%; Pred. No. 2e-16;
RESULT 168
ID ADS18408 standard; protein; 187 AA.
DE Drosophila sp. Rklp family member protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 18.5%; Score 222.5; DB 8; Length 187;
Best Local Similarity 38.6%; Pred. No. 2e-16;
RESULT 169
ID ADS18409 standard; protein; 220 AA.
DE Caenorhabditis elegans Rklp family member protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 18.4%; Score 222; DB 8; Length 220;
Best Local Similarity 33.1%; Pred. No. 2.8e-16;
RESULT 170
ID ADI34939 standard; protein; 186 AA.
DE Bovine PEBP protein sequence.
PN WO2004005931-A1.

PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 18.1%; Score 218.5; DB 8; Length 186;
Best Local Similarity 33.3%; Pred. No. 5.6e-16;
RESULT 171
ID AAB83148 standard; protein; 187 AA.
DE Mouse pepb-2 polypeptide.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 18.1%; Score 218.5; DB 4; Length 187;
Best Local Similarity 33.3%; Pred. No. 5.6e-16;
RESULT 172
ID AAB83150 standard; protein; 187 AA.
DE Mouse pepb-2 21 kDa form.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 18.1%; Score 218.5; DB 4; Length 187;
Best Local Similarity 33.3%; Pred. No. 5.6e-16;
RESULT 173
ID AAB66542 standard; protein; 202 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26418.
PN WO20011042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 18.0%; Score 216.5; DB 4; Length 202;
Best Local Similarity 28.0%; Pred. No. 1.1e-15;
RESULT 174
ID ABB30879 standard; protein; 187 AA.
DE Mouse nerve related protein.
PN JP2002176881-A.
PD 25-JUN-2002.
PA (OSHI) OSHIYA Y.
Query Match 17.8%; Score 214; DB 5; Length 187;
Best Local Similarity 34.4%; Pred. No. 1.8e-15;
RESULT 175
ID ADS18407 standard; protein; 187 AA.
DE Murine PEBP protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 17.7%; Score 213; DB 8; Length 187;
Best Local Similarity 33.8%; Pred. No. 2.4e-15;
RESULT 176
ID ADS18406 standard; protein; 187 AA.
DE Human PEBP protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 17.5%; Score 211; DB 8; Length 187;
Best Local Similarity 33.8%; Pred. No. 4e-15;
RESULT 177
ID ABPE2845 standard; protein; 233 AA.
DE Human polypeptide SEQ ID NO 282.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 17.2%; Score 207.5; DB 5; Length 233;
Best Local Similarity 31.8%; Pred. No. 1.4e-14;
RESULT 178
ID ABO14670 standard; protein; 186 AA.
DE Novel human protein #43.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 17.0%; Score 205; DB 6; Length 186;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 179
ID ADI34938 standard; protein; 186 AA.
DE Human PEBP protein sequence.
PN WO2004005931-A1.

PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 17.0%; Score 205; DB 8; Length 186;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 180
ID AAR27718 standard; protein; 187 AA.
DE HCNP precursor protein #2.
PN EP51816-A2.
PD 04-NOV-1992.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (OITK/) OITKA K.
PA (YAMA/) YAMAMOTO M.
Query Match 17.0%; Score 205; DB 2; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 181
ID AAR49943 standard; protein; 187 AA.
DE Human hippocampal cholinergic neurotrophic peptide precursor.
PN WO9405788-A1.
PD 17-MAR-1994.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (YAMA/) YAMAMOTO M.
Query Match 17.0%; Score 205; DB 2; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 182
ID AAR64268 standard; protein; 187 AA.
DE Phosphatidylethanolamine binding protein.
PN EP628631-A1.
PD 14-DEC-1994.
PA (ONOV) ONO PHARM CO LTD.
Query Match 17.0%; Score 205; DB 2; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 183
ID AAR21677 standard; protein; 187 AA.
DE Human phosphoethanolamine binding protein (PEBP).
PN WO200218623-A2.
PD 07-MAR-2002.
PA (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
Query Match 17.0%; Score 205; DB 5; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 184
ID ABO14671 standard; protein; 187 AA.
DE Novel human protein #44.
PN WO2003023002-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 17.0%; Score 205; DB 6; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 185
ID ADJ68662 standard; protein; 187 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID468.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 17.0%; Score 205; DB 7; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 186
ID ABR81481 standard; protein; 187 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO59001, SEQ:3817.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 17.0%; Score 205; DB 8; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 187
ID ADP23651 standard; protein; 187 AA.
DE PRO polypeptide SEQ ID NO:1029.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 17.0%; Score 205; DB 8; Length 187;
Best Local Similarity 33.1%; Pred. No. 1.9e-14;
RESULT 188

ID AAE25747 standard; protein; 176 AA.
DE Rice FT homologue protein from clone rls24.pk0017.c7.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 17.0%; Score 204.5; DB 5; Length 176;
Best Local Similarity 31.3%; Pred. No. 2e-14;
RESULT 189
ID ADR04263 standard; protein; 176 AA.
DE Rice FT homologue protein SEQ ID NO:30.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 17.0%; Score 204.5; DB 8; Length 176;
Best Local Similarity 31.3%; Pred. No. 2e-14;
RESULT 190
ID ADI34941 standard; protein; 121 AA.
DE Mouse CDP orthologue sequence.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 16.9%; Score 203; DB 8; Length 121;
Best Local Similarity 43.0%; Pred. No. 1.8e-14;
RESULT 191
ID AAE25750 standard; protein; 172 AA.
DE Soybean FT homologue protein #1.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 16.8%; Score 202.5; DB 5; Length 172;
Best Local Similarity 34.4%; Pred. No. 3.3e-14;
RESULT 192
ID ADR04269 standard; protein; 172 AA.
DE Soybean FT homologue protein SEQ ID NO:36.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 16.8%; Score 202.5; DB 8; Length 172;
Best Local Similarity 34.4%; Pred. No. 3.3e-14;
RESULT 193
ID ADJ68454 standard; protein; 140 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID260.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 16.8%; Score 202; DB 7; Length 140;
Best Local Similarity 34.7%; Pred. No. 2.8e-14;
RESULT 194
ID AAE25753 standard; protein; 180 AA.
DE Wheat FT homologue protein from clone wdk2c.pk012.017.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 16.2%; Score 194.5; DB 5; Length 180;
Best Local Similarity 29.4%; Pred. No. 2.9e-13;
RESULT 195
ID ADR04275 standard; protein; 180 AA.
DE Wheat FT homologue protein SEQ ID NO:42.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 16.2%; Score 194.5; DB 8; Length 180;
Best Local Similarity 29.4%; Pred. No. 2.9e-13;
RESULT 196
ID AAE25759 standard; protein; 158 AA.
DE Corn FT homologue protein from clone ctain.pk0058.d11b.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.

Query Match 16.0%; Score 193; DB 5; Length 158;
Best Local Similarity 40.5%; Pred. No. 3.5e-13;
RESULT 197
ID ADR04287 standard; protein; 158 AA.
DE Corn FT homologue protein SEQ ID NO:54.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 16.0%; Score 193; DB 8; Length 158;
Best Local Similarity 40.5%; Pred. No. 3.5e-13;
RESULT 198
ID AAE25735 standard; protein; 180 AA.
DE Garden balsam FT homologue protein from clone ids.pk0031.a5.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 16.0%; Score 193; DB 5; Length 180;
Best Local Similarity 34.1%; Pred. No. 4.2e-13;
RESULT 199
ID ADR04239 standard; protein; 180 AA.
DE Garden balsam FT homologue protein SEQ ID NO:6.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 16.0%; Score 193; DB 8; Length 180;
Best Local Similarity 34.1%; Pred. No. 4.2e-13;
RESULT 200
ID AAB83149 standard; protein; 173 AA.
DE Mouse pepb-2 20 kDa form.
PN WO200123424-A1.
PD 05-APR-2001.
PA (MONU) UNIV MONASH.
Query Match 16.0%; Score 192.5; DB 4; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.6e-13;
RESULT 201
ID AAE25739 standard; protein; 180 AA.
DE Corn FT homologue protein #2.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.9%; Score 192; DB 5; Length 180;
Best Local Similarity 36.3%; Pred. No. 5.5e-13;
RESULT 202
ID ADR04247 standard; protein; 180 AA.
DE Corn FT homologue protein SEQ ID NO:14.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 15.9%; Score 192; DB 8; Length 180;
Best Local Similarity 36.3%; Pred. No. 5.5e-13;
RESULT 203
ID ABE69361 standard; protein; 169 AA.
DE Human polypeptide SEQ ID NO 1408.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 15.8%; Score 190; DB 5; Length 169;
Best Local Similarity 34.3%; Pred. No. 8.5e-13;
RESULT 204
ID ABB62918 standard; protein; 179 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15546.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PR CORP NY.
Query Match 15.5%; Score 186.5; DB 4; Length 179;
Best Local Similarity 35.6%; Pred. No. 2.3e-12;
RESULT 205
ID AAE25734 standard; protein; 174 AA.
DE Balsam pear FT homologue protein.
PN WO200244390-A2.

PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.4%; Score 185.5; DB 5; Length 174;
Best Local Similarity 38.5%; Pred. No. 2.9e-12;
RESULT 206
ID ADR04237 standard; protein; 174 AA.
DE Balsam pear FT homologue protein SEQ ID NO:4.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.4%; Score 185.5; DB 8; Length 174;
Best Local Similarity 38.5%; Pred. No. 2.9e-12;
RESULT 207
ID ADR94938 standard; protein; 178 AA.
DE Japanese rice Nipponbare variety flowering-related RFT1 protein.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 15.4%; Score 185; DB 8; Length 178;
Best Local Similarity 33.3%; Pred. No. 3.4e-12;
RESULT 208
ID ADR94935 standard; protein; 178 AA.
DE Indian rice Kasalath variety flowering-related RFT1 protein.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 15.2%; Score 183; DB 8; Length 178;
Best Local Similarity 33.3%; Pred. No. 5.7e-12;
RESULT 209
ID AAG31274 standard; protein; 175 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37530.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 15.1%; Score 182; DB 3; Length 175;
Best Local Similarity 36.2%; Pred. No. 7.2e-12;
RESULT 210
ID AAE25741 standard; protein; 177 AA.
DE Corn FT homologue protein from clone p0081.chcad07r.
PN WO200424390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.1%; Score 182; DB 5; Length 177;
Best Local Similarity 32.9%; Pred. No. 7.3e-12;
RESULT 211
ID ADR04251 standard; protein; 177 AA.
DE Corn FT homologue protein SEQ ID NO:18.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.1%; Score 182; DB 8; Length 177;
Best Local Similarity 32.9%; Pred. No. 7.3e-12;
RESULT 212
ID AAE24557 standard; protein; 179 AA.
DE Floral developmental protein related rice protein.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.1%; Score 182; DB 5; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 213
ID ABG31338 standard; protein; 179 AA.
DE Rice Hd3a protein #2.
PN WO200242475-A1.
PD 30-MAY-2002.
PA (NAG-) NAT INST AGROBIOLOGICAL SCI.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 15.1%; Score 182; DB 5; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;

Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 214
ID ABG31337 standard; protein; 179 AA.
DE Rice Hd3a protein #1.
PN WO200242475-A1.
PD 30-MAY-2002.
PA (NAG-) NAT INST AGROBIOLOGICAL SCI.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
Query Match 15.1%; Score 182; DB 5; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 215
ID ADR94939 standard; protein; 179 AA.
DE Indian rice Kasalath variety flowering-related Hd3a protein.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 15.1%; Score 182; DB 8; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 216
ID ADR94940 standard; protein; 179 AA.
DE Japanese rice Nipponbare variety flowering-related Hd3a protein.
PN JP2004089036-A.
PD 25-MAR-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
Query Match 15.1%; Score 182; DB 8; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 217
ID ADR04295 standard; protein; 179 AA.
DE Rice FT homologue protein SEQ ID NO:62.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 15.1%; Score 182; DB 8; Length 179;
Best Local Similarity 32.9%; Pred. No. 7.5e-12;
RESULT 218
ID ABB6541 standard; protein; 211 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 26415.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.1%; Score 181.5; DB 4; Length 211;
Best Local Similarity 34.1%; Pred. No. 1.1e-11;
RESULT 219
ID ABB61522 standard; protein; 210 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11358.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 15.0%; Score 181; DB 4; Length 210;
Best Local Similarity 33.3%; Pred. No. 1.2e-11;
RESULT 220
ID ADU33451 standard; protein; 177 AA.
DE Festuca arundinacea floral development protein SEQ ID NO:26.
PN WO2004022755-A2.
PD 18-MAR-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 14.9%; Score 179; DB 8; Length 177;
Best Local Similarity 32.2%; Pred. No. 1.6e-11;
RESULT 221
ID ABG27458 standard; protein; 225 AA.
DE Novel human diagnostic protein #27449.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEO INC.
Query Match 14.7%; Score 177.5; DB 4; Length 225;
Best Local Similarity 34.7%; Pred. No. 3.3e-11;
RESULT 222

ID AAE25760 standard; protein; 174 AA.
DE Rice FT homologue protein from clone rblm1c.pk001.a6.fis.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.6%; Score 175.5; DB 5; Length 174;
Best Local Similarity 27.5%; Pred. No. 3.9e-11;
RESULT 223
ID ADR04289 standard; protein; 174 AA.
DE Rice FT homologue protein SEQ ID NO:56.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.6%; Score 175.5; DB 8; Length 174;
Best Local Similarity 27.5%; Pred. No. 3.9e-11;
RESULT 224
ID ABB67136 standard; protein; 176 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28200.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 14.6%; Score 175.5; DB 4; Length 176;
Best Local Similarity 33.8%; Pred. No. 4e-11;
RESULT 225
ID AAE25752 standard; protein; 173 AA.
DE Soybean FT homologue protein #2.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.0%; Score 169; DB 5; Length 173;
Best Local Similarity 35.9%; Pred. No. 2.1e-10;
RESULT 226
ID ADR04273 standard; protein; 173 AA.
DE Soybean FT homologue protein SEQ ID NO:40.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.0%; Score 169; DB 8; Length 173;
Best Local Similarity 35.9%; Pred. No. 2.1e-10;
RESULT 227
ID AAE25737 standard; protein; 172 AA.
DE Corn FT homologue protein from clone cc71se-b.pk0003.h10.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.0%; Score 168.5; DB 5; Length 172;
Best Local Similarity 29.2%; Pred. No. 2.4e-10;
RESULT 228
ID ADR04243 standard; protein; 172 AA.
DE Corn FT homologue protein SEQ ID NO:10.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.0%; Score 168.5; DB 8; Length 172;
Best Local Similarity 29.2%; Pred. No. 2.4e-10;
RESULT 229
ID AAE25736 standard; protein; 173 AA.
DE Corn FT homologue protein #1.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.0%; Score 168.5; DB 5; Length 173;
Best Local Similarity 33.3%; Pred. No. 2.4e-10;
RESULT 230
ID ADR04241 standard; protein; 173 AA.
DE Corn FT homologue protein SEQ ID NO:8.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.0%; Score 168.5; DB 8; Length 173;
Best Local Similarity 33.3%; Pred. No. 2.4e-10;
RESULT 231
ID ADR04240 standard; protein; 177 AA.
DE Corn FT homologue protein from clone p0014.ctush42r.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.0%; Score 168.5; DB 5; Length 177;
Best Local Similarity 31.1%; Pred. No. 2.5e-10;
RESULT 232
ID ADR04249 standard; protein; 177 AA.
DE Corn FT homologue protein SEQ ID NO:16.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.0%; Score 168.5; DB 8; Length 177;
Best Local Similarity 31.1%; Pred. No. 2.5e-10;
RESULT 233
ID ADC03498 standard; protein; 184 AA.
DE Rice flowering time-related protein #41.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.9%; Score 167.5; DB 7; Length 184;
Best Local Similarity 31.9%; Pred. No. 3.4e-10;
RESULT 234
ID AAE25733 standard; protein; 150 AA.
DE Peruvian lily FT homologue protein from clone eallc.pk006.e6.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 13.8%; Score 166; DB 5; Length 150;
Best Local Similarity 39.4%; Pred. No. 3.8e-10;
RESULT 235
ID ADR04235 standard; protein; 150 AA.
DE Peruvian lily FT homologue protein SEQ ID NO:2.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 13.8%; Score 166; DB 8; Length 150;
Best Local Similarity 39.4%; Pred. No. 3.8e-10;
RESULT 236
ID ADQ30847 standard; protein; 173 AA.
DE Pea floral development protein PEFRLC.
PN EPI439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 13.7%; Score 165.5; DB 8; Length 173;
Best Local Similarity 27.2%; Pred. No. 5.3e-10;
RESULT 237
ID AAE25738 standard; protein; 174 AA.
DE Corn FT homologue protein from clone ccoln.pk0037.d10.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 13.7%; Score 165; DB 5; Length 174;
Best Local Similarity 34.4%; Pred. No. 6.1e-10;
RESULT 238
ID ADR04245 standard; protein; 174 AA.
DE Corn FT homologue protein SEQ ID NO:12.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 13.7%; Score 165; DB 8; Length 174;
Best Local Similarity 34.4%; Pred. No. 6.1e-10;
RESULT 239
ID ABB80315 standard; protein; 174 AA.
DE CRTL.
PN WO2003076612-A1.

Query Match 14.0%; Score 168.5; DB 8; Length 173;
Best Local Similarity 33.3%; Pred. No. 2.4e-10;
RESULT 231
ID AAE25740 standard; protein; 177 AA.
DE Corn FT homologue protein from clone p0014.ctush42r.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 14.0%; Score 168.5; DB 5; Length 177;
Best Local Similarity 31.1%; Pred. No. 2.5e-10;
RESULT 232
ID ADR04249 standard; protein; 177 AA.
DE Corn FT homologue protein SEQ ID NO:16.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 14.0%; Score 168.5; DB 8; Length 177;
Best Local Similarity 31.1%; Pred. No. 2.5e-10;
RESULT 233
ID ADC03498 standard; protein; 184 AA.
DE Rice flowering time-related protein #41.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.9%; Score 167.5; DB 7; Length 184;
Best Local Similarity 31.9%; Pred. No. 3.4e-10;
RESULT 234
ID AAE25733 standard; protein; 150 AA.
DE Peruvian lily FT homologue protein from clone eallc.pk006.e6.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 13.8%; Score 166; DB 5; Length 150;
Best Local Similarity 39.4%; Pred. No. 3.8e-10;
RESULT 235
ID ADR04235 standard; protein; 150 AA.
DE Peruvian lily FT homologue protein SEQ ID NO:2.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 13.8%; Score 166; DB 8; Length 150;
Best Local Similarity 39.4%; Pred. No. 3.8e-10;
RESULT 236
ID ADQ30847 standard; protein; 173 AA.
DE Pea floral development protein PEFRLC.
PN EPI439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 13.7%; Score 165.5; DB 8; Length 173;
Best Local Similarity 27.2%; Pred. No. 5.3e-10;
RESULT 237
ID AAE25738 standard; protein; 174 AA.
DE Corn FT homologue protein from clone ccoln.pk0037.d10.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 13.7%; Score 165; DB 5; Length 174;
Best Local Similarity 34.4%; Pred. No. 6.1e-10;
RESULT 238
ID ADR04245 standard; protein; 174 AA.
DE Corn FT homologue protein SEQ ID NO:12.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 13.7%; Score 165; DB 8; Length 174;
Best Local Similarity 34.4%; Pred. No. 6.1e-10;
RESULT 239
ID ABB80315 standard; protein; 174 AA.
DE CRTL.
PN WO2003076612-A1.

PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match
Best Local Similarity 13.6%; Score 164; DB 7; Length 174;
PD 21-OCT-1999.
ID AAY49098 standard; protein; 175 AA.
DE Amino acid sequence encoded by the flowering locus T gene.
PN W09953070-A1.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match
Best Local Similarity 13.6%; Score 164; DB 2; Length 175;
PD 23-MAY-2000.
ID AAB12459 standard; protein; 175 AA.
DE Arabidopsis thaliana protein sequence SEQ ID NO:1.
PN JF2000138250-A.
PA (TORA) TORAY IND INC.
Query Match
Best Local Similarity 13.6%; Score 164; DB 3; Length 175;
PD 06-SEP-2000.
ID AAG43545 standard; protein; 175 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57194.
PN EP1033405-A2.
Query Match
Best Local Similarity 13.6%; Score 164; DB 3; Length 175;
PD 06-SEP-2000.
ID AAG09536 standard; protein; 175 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7508.
PN EP1033405-A2.
Query Match
Best Local Similarity 13.6%; Score 164; DB 3; Length 175;
PD 06-SEP-2000.
ID AAB24556 standard; protein; 175 AA.
DE Arabidopsis thaliana TFL1-like protein.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.6%; Score 164; DB 5; Length 175;
PD 06-SEP-2000.
ID AOC77597 standard; protein; 175 AA.
DE A. thaliana flowering locus T (FT).
PN US2003093835-A1.
PD 15-MAY-2003.
PA (WEIG) WEIGEL D.
PA (AHNUJ) AHN J H.
Query Match
Best Local Similarity 13.6%; Score 164; DB 7; Length 175;
PD 06-SEP-2000.
ID ABB80318 standard; protein; 175 AA.
DE FT.
PN W02003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match
Best Local Similarity 13.6%; Score 164; DB 7; Length 175;
PD 06-SEP-2000.
ID ADR04294 standard; protein; 175 AA.
DE Arabidopsis thaliana FT homologue protein SEQ ID NO:61.
PN W02004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.6%; Score 164; DB 8; Length 175;
PD 06-SEP-2000.
ID AAG45544 standard; protein; 201 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57193.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.6%; Score 164; DB 3; Length 201;
PD 06-SEP-2000.
ID AAG09535 standard; protein; 202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7507.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.6%; Score 164; DB 3; Length 202;
PD 06-SEP-2000.
ID AAG31275 standard; protein; 107 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37531.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 13.4%; Score 161; DB 3; Length 107;
PD 06-SEP-2000.
ID AAE25754 standard; protein; 180 AA.
DE Wheat FT homologue protein from clone wdk9n1.pk001.o20.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.4%; Score 161; DB 5; Length 180;
PD 06-SEP-2000.
ID ADR04277 standard; protein; 180 AA.
DE Wheat FT homologue protein SEQ ID NO:44.
PN W02004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.4%; Score 161; DB 8; Length 180;
PD 06-SEP-2000.
ID AOC30869 standard; protein; 173 AA.
DE Pea floral development protein PEF1Lc variant #1.
PN EP1439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match
Best Local Similarity 13.3%; Score 160.5; DB 8; Length 173;
PD 06-SEP-2000.
ID AAE25762 standard; protein; 174 AA.
DE Rice FT homologue protein from clone rtr9n.pk001.d1.f1s.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.3%; Score 160; DB 5; Length 174;
PD 06-SEP-2000.
ID ADR04293 standard; protein; 174 AA.
DE Rice FT homologue protein SEQ ID NO:60.
PN W02004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match
Best Local Similarity 13.3%; Score 160; DB 8; Length 174;
PD 06-SEP-2000.
ID AOC30870 standard; protein; 173 AA.
DE Pea floral development protein PEF1Lc variant #2.
PN EP1439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match
Best Local Similarity 13.2%; Score 159.5; DB 8; Length 173;
PD 06-SEP-2000.
ID AOC77635 standard; protein; 176 AA.
DE A. thaliana FT/TFL1 4th exon chimera.
PN US2003093835-A1.

PA (WEIG/) WEIGEL D.
DE (AHHU/) AHN J H.
Query Match 13.2%; Score 158.5; DB 7; Length 176;
Best Local Similarity 36.0%; Pred. No. 3.4e-09;
RESULT 258
ID AAE38277 standard; protein; 276 AA.
DE Rice enhanced yield protein, FT.
PN WO2003048319-A2.
PD 12-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 13.1%; Score 157.5; DB 6; Length 276;
Best Local Similarity 31.6%; Pred. No. 8.2e-09;
RESULT 259
ID ABB80317 standard; protein; 173 AA.
DE FRD1.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIPOLIUM AS.
Query Match 12.8%; Score 154.5; DB 7; Length 173;
Best Local Similarity 28.0%; Pred. No. 9.5e-09;
RESULT 260
ID ADQ30845 standard; protein; 174 AA.
DE Pea floral development protein PetFla.
PN EPI439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 12.7%; Score 153.5; DB 8; Length 174;
Best Local Similarity 33.6%; Pred. No. 1.2e-08;
RESULT 261
ID AAE25742 standard; protein; 173 AA.
DE Corn FT homologue protein from clone p0104.cabak14rb.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.7%; Score 153; DB 5; Length 173;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
RESULT 262
ID ADR04253 standard; protein; 173 AA.
DE Corn FT homologue protein SEQ ID NO:20.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 12.7%; Score 153; DB 8; Length 173;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
RESULT 263
ID AAE25758 standard; protein; 173 AA.
DE Rice cen-1-like protein, PDR2.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 12.6%; Score 152; DB 5; Length 173;
Best Local Similarity 31.7%; Pred. No. 1.8e-08;
RESULT 264
ID ABB80316 standard; protein; 173 AA.
DE FRD2.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIPOLIUM AS.
Query Match 12.6%; Score 152; DB 7; Length 173;
Best Local Similarity 31.7%; Pred. No. 1.8e-08;
RESULT 265
ID ADN74880 standard; protein; 173 AA.
DE Rice RCN1 protein used to delay the flowering stage of the plant segid 1.
PN JP2004089026-A.
PD 25-MAR-2004.
PA (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.
Query Match 12.6%; Score 152; DB 8; Length 173;
Best Local Similarity 31.7%; Pred. No. 1.8e-08;
RESULT 266
ID ADR04284 standard; protein; 173 AA.

DE Rice FT homologue amino acid sequence SEQ ID NO:51.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 12.6%; Score 152; DB 8; Length 173;
Best Local Similarity 31.7%; Pred. No. 1.8e-08;
RESULT 267
ID AB089793 standard; protein; 179 AA.
DE Novel human protein NOV8a.
PN WO2003031571-A2.
PD 17-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.6%; Score 152; DB 6; Length 179;
Best Local Similarity 26.5%; Pred. No. 1.3e-08;
RESULT 268
ID ADC10118 standard; protein; 187 AA.
DE Human NOVX polypeptide SEQ ID NO: 138.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.6%; Score 152; DB 7; Length 187;
Best Local Similarity 31.2%; Pred. No. 2e-08;
RESULT 269
ID AAG45546 standard; protein; 107 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57195.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.5%; Score 150; DB 3; Length 107;
Best Local Similarity 34.9%; Pred. No. 1.6e-08;
RESULT 270
ID AAG09537 standard; protein; 107 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7509.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 12.5%; Score 150; DB 3; Length 107;
Best Local Similarity 34.9%; Pred. No. 1.6e-08;
RESULT 271
ID ADI19120 standard; protein; 172 AA.
DE MdFFL (Malus x domestica TERMINAL FLOWER) protein.
PN US2003237109-A1.
PD 25-DEC-2003.
PA (NAG-) NANT AGRIC RES ORG JAPAN.
Query Match 12.5%; Score 150; DB 8; Length 172;
Best Local Similarity 27.2%; Pred. No. 3e-08;
RESULT 272
ID ADQ30868 standard; protein; 174 AA.
DE Pea floral development protein PetFla variant #3.
PN EPI439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 12.4%; Score 149.5; DB 8; Length 174;
Best Local Similarity 32.8%; Pred. No. 3.5e-08;
RESULT 273
ID ADQ30867 standard; protein; 174 AA.
DE Pea floral development protein PetFla variant #2.
PN EPI439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 12.4%; Score 149.5; DB 8; Length 174;
Best Local Similarity 32.8%; Pred. No. 3.5e-08;
RESULT 274
ID ABB80314 standard; protein; 175 AA.
DE SP.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIPOLIUM AS.
Query Match 12.3%; Score 148.5; DB 7; Length 175;
Best Local Similarity 31.3%; Pred. No. 4.6e-08;
RESULT 275
ID AAW13944 standard; protein; 181 AA.
DE Antirrhinum centroradialis protein.

PN W09710339-A1.
PD 20-MAR-1997.
PA (INNE-) INNES CENT JOHN.
Query Match 12.3%; Score 148; DB 2; Length 181;
Best Local Similarity 29.1%; Pred. No. 5.5e-08;
RESULT 276
ID ABB80311 standard; protein; 181 AA.
DE CEN.
PN W02003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 12.3%; Score 148; DB 7; Length 181;
Best Local Similarity 29.1%; Pred. No. 5.5e-08;
RESULT 277
ID AD018410 standard; protein; 181 AA.
DE Antirrhinum sp. CEN protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 12.3%; Score 148; DB 8; Length 181;
Best Local Similarity 29.1%; Pred. No. 5.5e-08;
RESULT 278
ID AAB50270 standard; protein; 172 AA.
DE Strawberry flowering regulation protein SEQ ID NO: 40.
PN W0200071722-A1.
PD 30-NOV-2000.
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
Query Match 12.3%; Score 147.5; DB 4; Length 172;
Best Local Similarity 27.2%; Pred. No. 5.9e-08;
RESULT 279
ID AAB50271 standard; protein; 172 AA.
DE Strawberry flowering regulation protein SEQ ID NO: 44.
PN W0200071722-A1.
PD 30-NOV-2000.
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
Query Match 12.3%; Score 147.5; DB 4; Length 172;
Best Local Similarity 27.2%; Pred. No. 5.9e-08;
RESULT 280
ID ABB80312 standard; protein; 175 AA.
DE CER2.
PN W02003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 12.3%; Score 147.5; DB 7; Length 175;
Best Local Similarity 30.1%; Pred. No. 6e-08;
RESULT 281
ID ADC03392 standard; protein; 163 AA.
DE Rice flowering time-related protein #16.
PN W02003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 12.2%; Score 147; DB 7; Length 163;
Best Local Similarity 28.9%; Pred. No. 6.2e-08;
RESULT 282
ID AAB50269 standard; protein; 173 AA.
DE Strawberry flowering regulation protein SEQ ID NO: 37.
PN W0200071722-A1.
PD 30-NOV-2000.
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
Query Match 12.2%; Score 147; DB 4; Length 173;
Best Local Similarity 28.1%; Pred. No. 6.7e-08;
RESULT 283
ID AAB50266 standard; protein; 173 AA.
DE Strawberry flowering regulation protein SEQ ID NO: 6.
PN W0200071722-A1.
PD 30-NOV-2000.
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
Query Match 12.1%; Score 145.5; DB 4; Length 173;
Best Local Similarity 27.8%; Pred. No. 1e-07;
RESULT 284
ID ABB80313 standard; protein; 175 AA.

DE CER4.
PN W02003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 12.0%; Score 144.5; DB 7; Length 175;
Best Local Similarity 30.1%; Pred. No. 1.3e-07;
RESULT 285
ID AD009334 standard; protein; 179 AA.
DE Novel human protein Nov8a.
PN US2004014056-A1.
PD 22-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (CATY/) CATERTON E.
PA (CHAN/) CHANT J S.
PA (CHAU/) CHAUDHURI A.
PA (EDIN/) EDINGER S.
PA (GERL/) GERLACH V.
PA (GIOT/) GIOT L.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLET I.
PA (OOIC/) OOI C E.
PA (PATY/) PATURAJAN M.
PA (RIEG/) RIEGER D K.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPFLER R J.
PA (ZERR/) ZERRHOSEN B D.
PA (ZHON/) ZHONG M.
Query Match 11.9%; Score 143; DB 8; Length 179;
Best Local Similarity 25.8%; Pred. No. 2e-07;
RESULT 286
ID AAE25751 standard; protein; 173 AA.
DE Soybean FT homologue protein from clone srr2c.pk002.07.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.7%; Score 141; DB 5; Length 173;
Best Local Similarity 31.5%; Pred. No. 3.2e-07;
RESULT 287
ID ADR04271 standard; protein; 173 AA.
DE Soybean FT homologue protein SEQ ID NO:38.
PN W02004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.7%; Score 141; DB 8; Length 173;
Best Local Similarity 31.5%; Pred. No. 3.2e-07;
RESULT 288
ID AAE25748 standard; protein; 173 AA.
DE Rice FT homologue protein from clone rrl.pk043.f9.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.6%; Score 140; DB 5; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.2e-07;
RESULT 289
ID AAE25743 standard; protein; 173 AA.
DE Corn FT homologue protein from clone pol18.chaag04rb.
PN W0200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.6%; Score 140; DB 5; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.2e-07;
RESULT 290
ID ADM74682 standard; protein; 173 AA.
DE Rice RCN2 protein used to delay the flowering stage of the plant SeqID 3.
PN JP2004089026-A.
PD 25-MAR-2004.

PA (XAGA-) KAGAKU GIUTSU SHINKO JICHOYAN.
Query Match 11.6%; Score 140; DB 8; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.2e-07;
RESULT 291
ID ADR04255 standard; protein; 173 AA.
DE Corn FT homologue protein SEQ ID NO:22.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.6%; Score 140; DB 8; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.2e-07;
RESULT 292
ID ADR04265 standard; protein; 173 AA.
DE Rice FT homologue protein SEQ ID NO:32.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 11.6%; Score 140; DB 8; Length 173;
Best Local Similarity 30.8%; Pred. No. 4.2e-07;
RESULT 293
ID AAR15223 standard; protein; 152 AA.
DE OV-16 antigen.
PN USN7644372-N.
PD 05-NOV-1991.
PA (USSH) NAT INST OF HEALTH.
Query Match 11.5%; Score 139; DB 2; Length 152;
Best Local Similarity 38.5%; Pred. No. 4.6e-07;
RESULT 294
ID ADC03484 standard; protein; 173 AA.
DE Rice flowering time-related protein #34.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 11.5%; Score 138; DB 7; Length 173;
Best Local Similarity 30.9%; Pred. No. 7.1e-07;
RESULT 295
ID ADS18411 standard; protein; 176 AA.
DE Arabidopsis sp. TFL1 protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 11.4%; Score 137.5; DB 8; Length 176;
Best Local Similarity 30.2%; Pred. No. 8.3e-07;
RESULT 296
ID AAM13945 standard; protein; 177 AA.
DE Arabidopsis terminal flower 1 protein.
PN WO9710339-A1.
PD 20-MAR-1997.
PA (INNE-) INNES CENT JOHN.
Query Match 11.4%; Score 137.5; DB 2; Length 177;
Best Local Similarity 30.2%; Pred. No. 8.3e-07;
RESULT 297
ID ABB80308 standard; protein; 177 AA.
DE TFL1.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 11.4%; Score 137.5; DB 7; Length 177;
Best Local Similarity 30.2%; Pred. No. 8.3e-07;
RESULT 298
ID ADC03386 standard; protein; 163 AA.
DE Rice flowering time-related protein #13.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 11.4%; Score 137; DB 7; Length 163;
Best Local Similarity 30.1%; Pred. No. 8.5e-07;
RESULT 299
ID ADRI4919 standard; protein; 172 AA.
DE Rosa sp flower bud formation suppressor SEQ ID NO:2.
PN WO2004070036-A1.
PD 19-AUG-2004.
PA (WAKT) WAKUAGA PHARM CO LTD.
Query Match 11.4%; Score 137; DB 8; Length 172;
Best Local Similarity 31.5%; Pred. No. 9.1e-07;
RESULT 300
ID ADJ33461 standard; protein; 174 AA.
DE Festuca arundinacea floral development protein SEQ ID NO:36.
PN WO2004022755-A2.
PD 18-MAR-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 11.3%; Score 135.5; DB 8; Length 174;
Best Local Similarity 32.8%; Pred. No. 1.4e-06;
RESULT 301
ID ABB80310 standard; protein; 178 AA.
DE BNTFL1-3.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 11.0%; Score 133; DB 7; Length 178;
Best Local Similarity 32.1%; Pred. No. 2.7e-06;
RESULT 302
ID ABB80309 standard; protein; 178 AA.
DE BNTFL1-1.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 11.0%; Score 133; DB 7; Length 178;
Best Local Similarity 32.1%; Pred. No. 2.7e-06;
RESULT 303
ID AAE25744 standard; protein; 128 AA.
DE Rice FT homologue protein from clone rpm1c.pk001.a6.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 10.8%; Score 130; DB 5; Length 128;
Best Local Similarity 30.2%; Pred. No. 3.8e-06;
RESULT 304
ID ADR04257 standard; protein; 128 AA.
DE Rice FT homologue protein SEQ ID NO:24.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 10.8%; Score 130; DB 8; Length 128;
Best Local Similarity 30.2%; Pred. No. 3.8e-06;
RESULT 305
ID ADQ30866 standard; protein; 106 AA.
DE Pea floral development protein PetFla variant #1.
PN EP1439233-A1.
PD 21-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR.
Query Match 10.8%; Score 129.5; DB 8; Length 106;
Best Local Similarity 32.7%; Pred. No. 3.3e-06;
RESULT 306
ID AAE25761 standard; protein; 104 AA.
DE Rice FT homologue protein from clone r10n.pk0022.h10.f1e.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 10.7%; Score 129; DB 5; Length 104;
Best Local Similarity 32.3%; Pred. No. 3.7e-06;
RESULT 307
ID ADR04291 standard; protein; 104 AA.
DE Rice FT homologue protein SEQ ID NO:58.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 10.7%; Score 129; DB 8; Length 104;

Best Local Similarity 32.3%; Pred. No. 3.7e-06;
RESULT 308
ID ABB60940 standard; protein, 173 AA.
DE Novel floral meristem identity protein LpCen.
PN WO200233091-A1.
PD 25-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 10.6%; Score 128; DB 5; Length 173;
Best Local Similarity 29.3%; Pred. No. 9.7e-06;
RESULT 309
ID ABB60933 standard; protein, 173 AA.
DE Novel floral meristem identity protein LpCEN.
PN WO200233091-A1.
PD 25-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 10.6%; Score 128; DB 5; Length 173;
Best Local Similarity 29.3%; Pred. No. 9.7e-06;
RESULT 310
ID ABB80295 standard; protein, 173 AA.
DE LpFEL.
PN WO2003076612-A1.
PD 18-SEP-2003.
PA (DLFT-) DLF TRIFOLIUM AS.
PA (RISO-) RISOE NAT LAB.
Query Match 10.6%; Score 128; DB 7; Length 173;
Best Local Similarity 29.3%; Pred. No. 9.7e-06;
RESULT 311
ID AAB24593 standard; protein, 23 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:219.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.3%; Score 124; DB 3; Length 23;
Best Local Similarity 10.0%; Pred. No. 1.7e-06;
RESULT 312
ID AD318412 standard; protein, 219 AA.
DE Yeast RKIP family member protein.
PN US2004180341-A1.
PD 16-SEP-2004.
PA (UYBR-) UNIV BROWN.
Query Match 10.2%; Score 122.5; DB 8; Length 219;
Best Local Similarity 28.2%; Pred. No. 5.7e-05;
RESULT 313
ID AAB24592 standard; protein, 24 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:218.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.0%; Score 121; DB 3; Length 24;
Best Local Similarity 10.0%; Pred. No. 4e-06;
RESULT 314
ID ADC77598 standard; protein, 136 AA.
DE A.thaliana terminal flower 1 (TFP1).
PN US2003093835-A1.
PD 15-MAY-2003.
PA (WEIG/) WEIGEL D.
PA (AANU/) AAN J H.
Query Match 10.0%; Score 120.5; DB 7; Length 136;
Best Local Similarity 34.9%; Pred. No. 5e-05;
RESULT 315
ID AD134916 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 316
ID AD134918 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 317
ID AD134926 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 318
ID AD134921 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 319
ID AD134911 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 320
ID AD134917 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 321
ID AD134907 standard; peptide, 22 AA.
DE Cardiovascular disorder plasma polypeptide (CPP) tryptic peptide.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 322
ID AD134924 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 323
ID AD134925 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 324
ID AD134930 standard; peptide, 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.9%; Score 119; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-06;
RESULT 325
ID AAB25745 standard; protein, 105 AA.
DE Rice FT homologue protein.
PN WO200244390-A2.
PD 06-JUN-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 9.9%; Score 119; DB 5; Length 105;
Best Local Similarity 31.2%; Pred. No. 5.2e-05;
RESULT 326
ID ADR04259 standard; protein; 105 AA.
DE Rice FM homologue protein SEQ ID NO:26.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 9.9%; Score 119; DB 8; Length 105;
Best Local Similarity 31.2%; Pred. No. 5.2e-05;
RESULT 327
ID ABG27456 standard; protein; 82 AA.
DE Novel human diagnostic protein #27447.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.8%; Score 118.5; DB 4; Length 82;
Best Local Similarity 41.3%; Pred. No. 4.2e-05;
RESULT 328
ID ADI34928 standard; peptide; 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.6%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 329
ID ADI34922 standard; peptide; 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.6%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 330
ID ADI34920 standard; peptide; 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.6%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 331
ID ADI34927 standard; peptide; 22 AA.
DE Human CPP peptide fragment.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.6%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 332
ID ADI34905 standard; peptide; 22 AA.
DE Cardiovascular disorder plasma polypeptide (CPP) cryptic peptide.
PN WO2004005931-A1.
PD 15-JAN-2004.
PA (GENE-) GENEPROT INC.
Query Match 9.6%; Score 115; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
RESULT 333
ID ABB04703 standard; protein; 197 AA.
DE Mycobacterium tuberculosis protein 38.
PN WO200244406-A2.
PD 06-JUN-2002.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 9.4%; Score 113.5; DB 5; Length 197;
Best Local Similarity 27.4%; Pred. No. 0.00052;
RESULT 334
ID AAU30772 standard; protein; 230 AA.
DE Novel human secreted protein #1263.
PN WO200179449-A2.
PD 25-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 9.3%; Score 111.5; DB 4; Length 230;
Best Local Similarity 31.2%; Pred. No. 0.0011;
RESULT 335
ID AAB24594 standard; protein; 20 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:220.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.8%; Score 106; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00016;
RESULT 336
ID ABB68134 standard; protein; 409 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31194.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.6%; Score 103; DB 4; Length 409;
Best Local Similarity 28.0%; Pred. No. 0.0022;
RESULT 337
ID ADC03372 standard; protein; 173 AA.
DE Rice flowering time-related protein #6.
PN WO2003000904-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 8.3%; Score 100; DB 7; Length 173;
Best Local Similarity 39.7%; Pred. No. 0.015;
RESULT 338
ID ABB04704 standard; protein; 201 AA.
DE Mycobacterium tuberculosis protein 39.
PN WO200244406-A2.
PD 06-JUN-2002.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 7.9%; Score 95; DB 5; Length 201;
Best Local Similarity 27.3%; Pred. No. 0.067;
RESULT 339
ID ABO61017 standard; protein; 229 AA.
DE Klebsiella pneumoniae polypeptide seqid 7534.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.7%; Score 93; DB 7; Length 229;
Best Local Similarity 24.7%; Pred. No. 0.14;
RESULT 340
ID ABB98239 standard; protein; 172 AA.
DE Wheat Scip-1 orthologue SEQ ID NO 10.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.7%; Score 92.5; DB 5; Length 172;
Best Local Similarity 24.1%; Pred. No. 0.1;
RESULT 341
ID ABB98237 standard; protein; 176 AA.
DE Maize Scip-1 orthologue SEQ ID NO 6.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.6%; Score 91.5; DB 5; Length 176;
Best Local Similarity 25.2%; Pred. No. 0.14;
RESULT 342
ID ADN18277 standard; protein; 551 AA.
DE Bacterial polypeptide #930.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.6%; Score 91.5; DB 8; Length 551;
Best Local Similarity 23.0%; Pred. No. 0.67;
RESULT 343
ID AAB24595 standard; protein; 17 AA.

DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:221.
PN WO200355937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.6%; Score 91; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0064;
RESULT 344
ID ADK16367 standard; protein; 179 AA.
DE Nanorarchaeum equitans cancer-associated (CA) protein #159.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 7.5%; Score 90; DB 8; Length 179;
Best Local Similarity 27.4%; Pred. No. 0.21;
RESULT 345
ID AAV11503 standard; protein; 120 AA.
DE Human 5' EST secreted protein SEQ ID NO 325.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST-) GENSET.
Query Match 7.4%; Score 89.5; DB 2; Length 120;
Best Local Similarity 26.5%; Pred. No. 0.14;
RESULT 346
ID AAW72901 standard; protein; 176 AA.
DE Mycobacterium tuberculosis antigen CFP19.
PN WO9844119-A1.
PD 08-OCT-1998.
PA (STAT-) STATENS SERUM INST.
Query Match 7.4%; Score 89.5; DB 2; Length 176;
Best Local Similarity 28.8%; Pred. No. 0.24;
RESULT 347
ID AAV21918 standard; protein; 176 AA.
DE Amino acid sequence of antigen CFP19.
PN WO9924577-A1.
PD 20-MAY-1999.
PA (STAT-) STATENS SERUM INST.
Query Match 7.4%; Score 89.5; DB 2; Length 176;
Best Local Similarity 28.8%; Pred. No. 0.24;
RESULT 348
ID AAB95630 standard; protein; 196 AA.
DE Human protein sequence SEQ ID NO:18356.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.4%; Score 89.5; DB 4; Length 196;
Best Local Similarity 26.5%; Pred. No. 0.27;
RESULT 349
ID ADU70364 standard; protein; 196 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2170.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 7.4%; Score 89.5; DB 7; Length 196;
Best Local Similarity 26.5%; Pred. No. 0.27;
RESULT 350
ID AAM39921 standard; protein; 348 AA.
DE Human polypeptide SEQ ID NO 3066.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 89.5; DB 4; Length 348;
Best Local Similarity 26.5%; Pred. No. 0.6;
RESULT 351
ID AAB47132 standard; protein; 380 AA.
DE CDIF-13, Incyte ID No. 333139CD1.
PN WO200119860-A2.
PD 22-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.4%; Score 89.5; DB 4; Length 380;
Best Local Similarity 26.5%; Pred. No. 0.68;
RESULT 352
ID ABP57772 standard; protein; 380 AA.
DE Tumour suppressor factor 41.80 polypeptide.
PN CN1345740-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 7.4%; Score 89.5; DB 5; Length 380;
Best Local Similarity 26.5%; Pred. No. 0.68;
RESULT 353
ID AAM41707 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 6638.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 89.5; DB 4; Length 389;
Best Local Similarity 26.5%; Pred. No. 0.7;
RESULT 354
ID ABB65449 standard; protein; 1945 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23139.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 7.4%; Score 89.5; DB 4; Length 1945;
Best Local Similarity 22.0%; Pred. No. 6.4;
RESULT 355
ID ABB98238 standard; protein; 174 AA.
DE Maize SCIP-1 orthologue SEQ ID NO 8.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.4%; Score 88.5; DB 5; Length 174;
Best Local Similarity 23.7%; Pred. No. 0.3;
RESULT 356
ID AAE25749 standard; protein; 87 AA.
DE Rice FT homologue protein from clone rrr9n.pk001.d1.
PN WO200244390-A2.
PD 06-JUN-2002.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 7.3%; Score 88; DB 5; Length 87;
Best Local Similarity 43.6%; Pred. No. 0.13;
RESULT 357
ID ADR04267 standard; protein; 87 AA.
DE Rice FT homologue protein SEQ ID NO:34.
PN WO2004067723-A2.
PD 12-AUG-2004.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.3%; Score 88; DB 8; Length 87;
Best Local Similarity 43.6%; Pred. No. 0.13;
RESULT 358
ID ABB98236 standard; protein; 167 AA.
DE Rice SCIP-1 orthologue SEQ ID NO 4.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.3%; Score 88; DB 5; Length 167;
Best Local Similarity 29.2%; Pred. No. 0.32;
RESULT 359
ID ADE59592 standard; protein; 174 AA.
DE Human Protein AAF28940, SEQ ID NO 5488.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 7.3%; Score 88; DB 7; Length 174;
Best Local Similarity 28.0%; Pred. No. 0.34;
RESULT 360
ID ADD47523 standard; protein; 174 AA.
DE Human Protein AAF28940, SEQ ID NO 13219.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 7.3%; Score 88; DB 7; Length 174;
Best Local Similarity 28.0%; Pred. No. 0.34;

RESULT 361
ID AAB25731 standard; protein; 267 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:120.
PN WO200043495-A2.
PD 27-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 88; DB 3; Length 267;
Best Local Similarity 28.0%; Pred. No. 0.62;
RESULT 362
ID AAB25677 standard; protein; 297 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:66.
PN WO200043495-A2.
PD 27-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 88; DB 3; Length 297;
Best Local Similarity 28.0%; Pred. No. 0.71;
RESULT 363
ID ADA5685 standard; protein; 297 AA.
DE Human secreted protein #138.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 88; DB 6; Length 297;
Best Local Similarity 28.0%; Pred. No. 0.71;
RESULT 364
ID ADA40705 standard; protein; 297 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 88; DB 6; Length 297;
Best Local Similarity 28.0%; Pred. No. 0.71;
RESULT 365
ID ABR52348 standard; protein; 1705 AA.
DE Protein relating to the invention SEQ ID NO: 37.
PN WO200257460-A2.
PD 25-JUL-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 7.3%; Score 87.5; DB 5; Length 1705;
Best Local Similarity 23.8%; Pred. No. 9;
RESULT 366
ID ADJ33452 standard; protein; 89 AA.
DE Lolium perenne floral development protein SEQ ID NO:27.
PN WO2004022755-A2.
PD 18-MAR-2004.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 7.2%; Score 87; DB 8; Length 89;
Best Local Similarity 38.6%; Pred. No. 0.18;
RESULT 367
ID AAB55378 standard; protein; 163 AA.
DE Propionibacterium acnes immunogenic protein #16274.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 87; DB 4; Length 163;
Best Local Similarity 23.2%; Pred. No. 0.41;
RESULT 368
ID ABM51897 standard; protein; 163 AA.
DE Propionibacterium acnes immunogenic polypeptide #16573.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 87; DB 6; Length 163;
Best Local Similarity 23.2%; Pred. No. 0.41;
RESULT 369
ID ABB98240 standard; protein; 165 AA.
DE wheat SCIP-1 orthologue SEQ ID NO 12.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.2%; Score 87; DB 5; Length 165;
Best Local Similarity 24.5%; Pred. No. 0.41;

RESULT 370
ID AAY37418 standard; protein; 156 AA.
DE Amino acid sequence of a Chlamydia trachomatis protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GENST) GENSET.
Query Match 7.2%; Score 86.5; DB 2; Length 156;
Best Local Similarity 26.0%; Pred. No. 0.44;
RESULT 371
ID ADM03940 standard; protein; 273 AA.
DE Human protein of the invention SEQ ID NO:2625.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 85.5; DB 7; Length 273;
Best Local Similarity 23.7%; Pred. No. 1.2;
RESULT 372
ID ABB98241 standard; protein; 165 AA.
DE wheat SCIP-1 orthologue SEQ ID NO 14.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.1%; Score 85; DB 5; Length 165;
Best Local Similarity 25.2%; Pred. No. 0.7;
RESULT 373
ID ADM4681 standard; protein; 182 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID559.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 7.0%; Score 84; DB 8; Length 182;
Best Local Similarity 20.9%; Pred. No. 1;
RESULT 374
ID ADR14031 standard; protein; 274 AA.
DE Human NF-kappaB pathway-associated protein SeqID32.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.9%; Score 83.5; DB 8; Length 274;
Best Local Similarity 21.4%; Pred. No. 2.1;
RESULT 375
ID AAB43849 standard; protein; 275 AA.
DE Human cancer associated protein sequence SEQ ID NO:1294.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 83.5; DB 3; Length 275;
Best Local Similarity 21.4%; Pred. No. 2.1;
RESULT 376
ID ADR90276 standard; peptide; 21 AA.
DE Thale cress intracellular transport/TFPI-related MFT peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIYUTSU SH.
Query Match 6.9%; Score 83; DB 8; Length 21;
Best Local Similarity 66.7%; Pred. No. 0.07;
RESULT 377
ID AAB43303 standard; protein; 595 AA.
DE Human ORFX ORF3067 polypeptide sequence SEQ ID NO:6134.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 83; DB 3; Length 595;
Best Local Similarity 23.6%; Pred. No. 6.9;
RESULT 378
ID ABB65177 standard; protein; 595 AA.
DE Hypoxia-regulated protein #51.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 6.9%; Score 83; DB 5; Length 595;
Best Local Similarity 23.6%; Pred. No. 6.9;
RESULT 379

ID ADP55469 standard; protein; 595 AA.
DE Human PRO protein sequence SEQ ID NO:1445.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 23.6%; Pred. No. 6.9; Length 595;
RESULT 380
ID ADP55467 standard; protein; 595 AA.
DE Human PRO protein sequence SEQ ID NO:1443.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GERTH) GENENTECH INC.
Query Match
Best Local Similarity 23.6%; Pred. No. 6.9; Length 595;
RESULT 381
ID ADN47114 standard; protein; 656 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID992.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 22.8%; Pred. No. 8.9; Length 656;
RESULT 382
ID ABB75664 standard; protein; 745 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 848.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 12; Length 745;
RESULT 383
ID ABB97464 standard; protein; 917 AA.
DE Novel human protein SEQ ID NO: 732.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 16; Length 917;
RESULT 384
ID ADE28187 standard; protein; 957 AA.
DE Human MDDT protein - SEQ ID 37.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 17; Length 957;
RESULT 385
ID ABB66143 standard; protein; 1297 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25221.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 32.5%; Pred. No. 26; Length 1297;
RESULT 386
ID AAG91425 standard; protein; 177 AA.
DE C glutamylum protein fragment SEQ ID NO: 5179.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 27.1%; Pred. No. 1.9; Length 177;
RESULT 387
ID ADA36340 standard; protein; 321 AA.
DE Acinetobacter baumannii protein #3501.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 21.6%; Pred. No. 5.7; Length 321;
RESULT 388
ID ADN72413 standard; protein; 464 AA.

DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 308.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
Query Match
Best Local Similarity 18.7%; Pred. No. 11; Length 464;
RESULT 389
ID ADN26391 standard; protein; 630 AA.
DE Bacterial polypeptide #9044.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 20.4%; Pred. No. 19; Length 630;
RESULT 390
ID ADQ96834 standard; protein; 648 AA.
DE Cytocarcinogen amino acid sequence.
PN CN1380415-A.
PD 20-NOV-2002.
PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
Query Match
Best Local Similarity 24.0%; Pred. No. 19; Length 648;
RESULT 391
ID ABU33994 standard; protein; 1042 AA.
DE Protein encoded by Prokaryotic essential gene #19521.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 22.7%; Pred. No. 37; Length 1042;
RESULT 392
ID AARI3050 standard; protein; 234 AA.
DE CD4-specific CDR-grafted light chain.
PN WO9109966-A.
PD 11-JUL-1991.
PA (ORTH) ORTHO PHARM CORP.
PA (CLIT) CELUTECH LTD.
Query Match
Best Local Similarity 25.3%; Pred. No. 5.4; Length 234;
RESULT 393
ID AAB24588 standard; protein; 83 AA.
DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:214.
PN WO200035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 69.6%; Pred. No. 1.5; Length 83;
RESULT 394
ID ADP58937 standard; protein; 279 AA.
DE Human polypeptide sequence SEQ ID NO:1345.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 26.7%; Pred. No. 7.9; Length 279;
RESULT 395
ID AAG45536 standard; protein; 354 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57182.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 24.0%; Pred. No. 12; Length 354;
RESULT 396
ID AAG45535 standard; protein; 406 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57181.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 24.0%; Pred. No. 15; Length 406;

RESULT 397
 ID AAG45534 standard; protein; 454 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 57180.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 3; Length 454;
 RESULT 398
 ID ABB91430 standard; protein; 454 AA.
 DE Herbicidally active polypeptide SEQ ID NO 641.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (PARB) BAYER AG.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 5; Length 454;
 RESULT 399
 ID ADN73975 standard; protein; 454 AA.
 DE Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 1870.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPOSEIGN NV.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 8; Length 454;
 RESULT 400
 ID ADR86325 standard; protein; 601 AA.
 DE Aspergillus fumigatus essential gene protein #375.
 PN WO2004067709-A2.
 PD 12-AUG-2004.
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 8; Length 601;
 RESULT 401
 ID AAW37098 standard; protein; 875 AA.
 DE Murine endothelial PAS domain protein 1 (EPAS1).
 PN US5695963-A.
 PD 09-DEC-1997.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 2; Length 875;
 RESULT 402
 ID AD062812 standard; protein; 1062 AA.
 DE Pseudomonas fluorescens salitracin protein SacB.
 PN WO2004056998-A1.
 PD 08-JUL-2004.
 PA (PHAR-) PHARMA MAR SA.
 PA (RUPF/) RUPFLES G K.
 Query Match
 Best Local Similarity 6.5%; Score 78; DB 8; Length 1062;
 RESULT 403
 ID AAR80616 standard; protein; 232 AA.
 DE Anti-human IL-4 humanised Mab h25D2-9 mature light chain.
 PN WO9524481-A2.
 PD 14-SEP-1995.
 PA (SCHE) SCHERING CORP.
 Query Match
 Best Local Similarity 6.4%; Score 77.5; DB 2; Length 232;
 RESULT 404
 ID AAY35525 standard; protein; 110 AA.
 DE Chlamydia pneumoniae transmembrane protein sequence.
 PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GEST) GENSET.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 2; Length 110;
 RESULT 405
 ID AAG04416 standard; protein; 354 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 435.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 3; Length 354;
 RESULT 406
 ID AAG04415 standard; protein; 407 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 434.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 3; Length 407;
 RESULT 407
 ID AAG04414 standard; protein; 455 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 433.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 3; Length 455;
 RESULT 408
 ID AAY14130 standard; protein; 579 AA.
 DE Human IL-1RD8 protein sequence.
 PN WO9919480-A2.
 PD 22-APR-1999.
 PA (SCHE) SCHERING CORP.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 2; Length 579;
 RESULT 409
 ID AAE16566 standard; protein; 579 AA.
 DE Human interleukin-1 receptor DMAX designation 8 (IL-1RD8) protein #1.
 PN US6326472-B1.
 PD 04-DEC-2001.
 PA (SCHE) SCHERING CORP.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 5; Length 579;
 RESULT 410
 ID ADB31953 standard; protein; 579 AA.
 DE Human interleukin-1 receptor DMAX designation 8 (IL-1RD8) #1.
 PN US2003055218-A1.
 PD 20-MAR-2003.
 PA (TIMA/) TIMANUS J C.
 PA (DEBE/) ANTONIUS DEBERTS J E M.
 PA (SANA/) SANA T R.
 PA (BAZA/) BAZAN J F.
 PA (KAST/) KASTLEIN R A.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 7; Length 579;
 RESULT 411
 ID ADG22680 standard; protein; 602 AA.
 DE Cyanophage S-2L encoded protein #425.
 PN FR2839079-A1.
 PD 31-OCT-2003.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT SEQUENCAGE GRP INTERE.
 PA (GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 8; Length 602;
 RESULT 412
 ID ABJ25467 standard; protein; 1275 AA.
 DE Aspergillus fumigatus essential gene protein #125.
 PN WO200286090-A2.
 PD 31-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 6.4%; Score 77; DB 6; Length 1275;
 RESULT 413
 ID AAB24590 standard; protein; 21 AA.
 DE Human secreted protein sequence encoded by gene 46 SEQ ID NO:216.
 PN WO200035937-A1.
 PD 22-JUN-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 6.4%; Score 76.5; DB 3; Length 21;
 RESULT 414
 ID AAY97743 standard; protein; 168 AA.
 DE H. annus SCIP-1 protein sequence.
 PN WO200136464-A2.
 PD 25-MAY-2001.
 PA (PION-) PIONEER HI-BRED INT INC.

PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 76.5; DB 4; Length 168;
Best Local Similarity 24.1%; Pred. No. 6.6;
RESULT 415
ID ABB98242 standard; protein; 168 AA.
DE Sunflower SCIP-1 SEQ ID NO 16.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 6.4%; Score 76.5; DB 5; Length 168;
Best Local Similarity 24.1%; Pred. No. 6.6;
RESULT 416
ID AAY92341 standard; protein; 321 AA.
DE Human cancer associated antigen precursor from clone NY-REN-57.
PN W0200020587-A2.
PD 13-APR-2000.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 6.4%; Score 76.5; DB 3; Length 321;
Best Local Similarity 20.7%; Pred. No. 16;
RESULT 417
ID ABB61503 standard; protein; 1137 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11301.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 76.5; DB 4; Length 1137;
Best Local Similarity 21.8%; Pred. No. 91;
RESULT 418
ID ABB61547 standard; protein; 1246 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11433.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 76.5; DB 4; Length 1246;
Best Local Similarity 21.8%; Pred. No. 1e+02;
RESULT 419
ID ADS42670 standard; protein; 268 AA.
DE Bacterial polypeptide #21100.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 6.3%; Score 76; DB 8; Length 268;
Best Local Similarity 20.4%; Pred. No. 14;
RESULT 420
ID ADC24087 standard; protein; 312 AA.
DE Protein sequence (SeqID 354) exhibiting nitrilase activity.
PN W02003000840-A2.
PD 03-JAN-2003.
PA (DIVE-) DIVERSA CORP.
PA (MADD) MADDEN D.
Query Match 6.3%; Score 76; DB 7; Length 312;
Best Local Similarity 27.6%; Pred. No. 18;
RESULT 421
ID ADH36188 standard; protein; 312 AA.
DE Chemical process monitoring-related nitrilase protein sequence SeqID354.
PN W02003098187-A2.
PD 27-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 6.3%; Score 76; DB 8; Length 312;
Best Local Similarity 27.6%; Pred. No. 18;
RESULT 422
ID ADG93887 standard; protein; 312 AA.
DE Nitrilase enzyme amino acid sequence SeqID354.
PN W02003097810-A2.
PD 27-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 6.3%; Score 76; DB 8; Length 312;
Best Local Similarity 27.6%; Pred. No. 18;
RESULT 423

ID ADI62486 standard; protein; 312 AA.
DE Nitrilase polypeptide #177.
PN W02003106415-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 6.3%; Score 76; DB 8; Length 312;
Best Local Similarity 27.6%; Pred. No. 18;
RESULT 424
ID ADI64607 standard; protein; 312 AA.
DE Nitrilase seq id 178.
PN US2004014195-A1.
PD 22-JAN-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 6.3%; Score 76; DB 8; Length 312;
Best Local Similarity 27.6%; Pred. No. 18;
RESULT 425
ID AAM65990 standard; protein; 351 AA.
DE Photornhabdus luminescens protein sequence #2187.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.3%; Score 76; DB 6; Length 351;
Best Local Similarity 26.7%; Pred. No. 21;
RESULT 426
ID ADD47825 standard; protein; 748 AA.
DE Rat Protein AAB23030, SEQ ID NO 13521.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 76; DB 7; Length 748;
Best Local Similarity 21.0%; Pred. No. 59;
RESULT 427
ID ADD47829 standard; protein; 748 AA.
DE Rat Protein AAB23030, SEQ ID NO 13525.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.3%; Score 76; DB 7; Length 748;
Best Local Similarity 21.0%; Pred. No. 59;
RESULT 428
ID ABB64097 standard; protein; 1430 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19083.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 76; DB 4; Length 1430;
Best Local Similarity 24.5%; Pred. No. 1.4e+02;
RESULT 429
ID ABO26067 standard; protein; 1435 AA.
DE Aspergillus fumigatus essential gene protein #725.
PN W0200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 76; DB 6; Length 1435;
Best Local Similarity 22.5%; Pred. No. 1.4e+02;
RESULT 430
ID ABO6653 standard; protein; 159 AA.
DE Klebsiella pneumoniae polypeptide seqid 13170.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75.5; DB 7; Length 159;
Best Local Similarity 28.1%; Pred. No. 8;
RESULT 431
ID ADT91443 standard; protein; 816 AA.
DE Arabidopsis thaliana gene 21858 encoded protein.
PN US2004191850-A1.
PD 30-SEP-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.3%; Score 75.5; DB 8; Length 816;

Best Local Similarity 22.7%; Pred. No. 75;
RESULT 432
ID AD69650 standard; protein; 965 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1456.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.3%; Score 75.5; DB 7; Length 965;
Best Local Similarity 21.4%; Pred. No. 95;
RESULT 433
ID AAW1576 standard; protein; 1049 AA.
DE Human phosphatidylinositol 3-kinase PI3K-gamma.
PN DE4445562-C1.
PD 04-APR-1996.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 6.3%; Score 75.5; DB 2; Length 1049;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 434
ID AAW1577 standard; protein; 1050 AA.
DE Human phosphatidylinositol 3-kinase PI3K-gamma.
PN DE4445562-C1.
PD 04-APR-1996.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 6.3%; Score 75.5; DB 2; Length 1050;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 435
ID ADH68167 standard; protein; 1075 AA.
DE HA epitope tagged PI3K-gamma ATP binding site deletion protein.
PN US2003182669-A1.
PD 25-SEP-2003.
PA (ROCK/) ROCKMAN H A.
PA (PRAS/) NAGA PRASAD S V.
PA (LAPO/) LAPORTE S A.
PA (BARA/) BARAK L S.
PA (CARO/) CARON M G.
Query Match 6.3%; Score 75.5; DB 8; Length 1075;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 436
ID AAW23947 standard; protein; 1101 AA.
DE Human phosphoinositide 3OH-kinase p120 subunit.
PN WO9749818-A2.
PD 31-DEC-1997.
PA (ONYX-) ONYX PHARM.
Query Match 6.3%; Score 75.5; DB 2; Length 1101;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 437
ID AAW90089 standard; protein; 1101 AA.
DE Human G-protein regulated PI3K p120 adapter subunit protein.
PN US5856132-A.
PD 05-JAN-1999.
PA (ONYX-) ONYX PHARM.
Query Match 6.3%; Score 75.5; DB 2; Length 1101;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 438
ID AAY76803 standard; protein; 1101 AA.
DE Human p120 regulatory subunit protein sequence.
PN US6017763-A.
PD 25-JAN-2000.
PA (ONYX-) ONYX PHARM INC.
PA (BARR-) BABRAM INST.
Query Match 6.3%; Score 75.5; DB 3; Length 1101;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 439
ID AAU09689 standard; protein; 1101 AA.
DE Human p110gamma isoform of PI3-kinase.
PN WO200185986-A2.
PD 15-NOV-2001.
PA (ICOS-) ICOS CORP.
Query Match 6.3%; Score 75.5; DB 5; Length 1101;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 440
ID AD69536 standard; protein; 1102 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1342.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.3%; Score 75.5; DB 7; Length 1102;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 441
ID ADY96267 standard; protein; 1102 AA.
DE Human phosphoinositide-3-kinase gamma protein SEQ ID NO:2.
PN WO2004026285-A2.
PD 01-APR-2004.
PA (UYHE-) UNIV HEALTH NETWORK.
PA (AMGE-) AMGEN CANADA INC.
Query Match 6.3%; Score 75.5; DB 8; Length 1102;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 442
ID ADH68165 standard; protein; 1110 AA.
DE HA epitope tagged PI3K-gamma protein.
PN US2003182669-A1.
PD 25-SEP-2003.
PA (ROCK/) ROCKMAN H A.
PA (PRAS/) NAGA PRASAD S V.
PA (LAPO/) LAPORTE S A.
PA (BARA/) BARAK L S.
PA (CARO/) CARON M G.
Query Match 6.3%; Score 75.5; DB 8; Length 1110;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 443
ID AAG51134 standard; protein; 1639 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64867.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 75.5; DB 3; Length 1639;
Best Local Similarity 20.1%; Pred. No. 2e+02;
RESULT 444
ID AAG51133 standard; protein; 1689 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64866.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 75.5; DB 3; Length 1689;
Best Local Similarity 20.1%; Pred. No. 2e+02;
RESULT 445
ID AAG51132 standard; protein; 1772 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 64865.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.3%; Score 75.5; DB 3; Length 1772;
Best Local Similarity 20.1%; Pred. No. 2.2e+02;
RESULT 446
ID ADP56158 standard; protein; 2000 AA.
DE Human PRO protein sequence SEQ ID NO:2134.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GERTH) GENTECH INC.
Query Match 6.3%; Score 75.5; DB 8; Length 2000;
Best Local Similarity 32.1%; Pred. No. 2.6e+02;
RESULT 447
ID ABG79533 standard; protein; 2035 AA.
DE Human tumour suppressor protein #19.
PN WO200264775-A1.
PD 22-AUG-2002.
PA (BITON-) BIONOMICS LTD.
Query Match 6.3%; Score 75.5; DB 5; Length 2035;
Best Local Similarity 32.1%; Pred. No. 2.6e+02;
RESULT 448
ID ADQ96094 standard; protein; 2035 AA.
DE T cell activation associated protein #136.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASahi KASEI PHARMA CORP.
Query Match 6.3%; Score 75.5; DB 8; Length 2035;
Best Local Similarity 32.1%; Pred. No. 2.6e+02;

RESULT 449
ID ABR66316 standard; protein: 2035 AA.
DE Human prostatic carcinoma derived protein SEQ ID 170 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match
Best Local Similarity 32.1%; Pred. No. 2.6e+02; Length 2035;
RESULT 450
ID ADR6658 standard; protein: 2035 AA.
DE Human prostatic carcinoma derived protein SEQ ID 170 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILASKY C.
Query Match
Best Local Similarity 32.1%; Pred. No. 2.6e+02; Length 2035;
RESULT 451
ID ADR9075 standard; peptide: 21 AA.
DE Thale cress intracellular transport/TFLI-related TSF peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match
Best Local Similarity 61.9%; Pred. No. 0.57; Length 21;
RESULT 452
ID ABO60571 standard; protein: 164 AA.
DE Human genome derived single exon protein #6805.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENNY/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 23.7%; Pred. No. 9.5; Length 164;
RESULT 453
ID ABR39322 standard; protein: 299 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4167.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.2%; Score 75; DB 5; Length 299;
RESULT 454
ID ADS05031 standard; protein: 299 AA.
DE Staphylococcus epidermis polypeptide seqid 4326.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 19.0%; Pred. No. 22; Length 299;
RESULT 455
ID ADC96439 standard; protein: 410 AA.
DE E. faecium protein sequence SEQ ID 6066.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.2%; Score 75; DB 7; Length 410;
RESULT 456
ID ADS30218 standard; protein: 569 AA.
DE Bacterial polypeptide #19251.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 24.4%; Pred. No. 52; Length 569;
RESULT 457
ID ADJ35052 standard; protein: 651 AA.
DE Xylanase from an environmental sample seq id 268.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 22.8%; Pred. No. 63; Length 651;
RESULT 458
ID AAY34517 standard; protein: 670 AA.
DE Porphyromonas gingivalis protein PG55.
PN WO9929870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD.
Query Match
Best Local Similarity 20.3%; Score 75; DB 2; Length 670;
RESULT 459
ID AAY34390 standard; protein: 702 AA.
DE Porphyromonas gingivalis protein PG55.
PN WO9929870-A1.
PD 17-JUN-1999.
PA (CSLC-) CSL LTD.
Query Match
Best Local Similarity 20.3%; Pred. No. 70; Length 702;
RESULT 460
ID ABR93037 standard; protein: 980 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 32.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match
Best Local Similarity 21.8%; Pred. No. 1.1e+02; Length 980;
RESULT 461
ID ABR52844 standard; protein: 980 AA.
DE Protein sequence #SEQ ID 553.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 6.2%; Score 75; DB 6; Length 980;
RESULT 462
ID ADR62288 standard; protein: 980 AA.
DE Disease creating protein complex-derived protein #270.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 6.2%; Score 75; DB 7; Length 980;
RESULT 463
ID ADN18753 standard; protein: 980 AA.
DE Bacterial polypeptide #1406.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 21.8%; Pred. No. 1.1e+02; Length 980;
RESULT 464
ID ADN19282 standard; protein: 1041 AA.
DE Bacterial polypeptide #1935.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.6%; Pred. No. 1.2e+02;
RESULT 465
ID ABB71134 standard; protein; 1419 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40194.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.2%; Score 75; DB 4; Length 1419;
Pred. No. 1.8e+02;
RESULT 466
ID AAY56286 standard; protein; 236 AA.
DE HCV1 clone 25 antibody variable light chain protein sequence.
PN EP959136-A1.
PD 24-NOV-1999.
PA (INTR-) INTROGENE BV.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 3; Length 236;
Pred. No. 18;
RESULT 467
ID ADS25081 standard; protein; 311 AA.
DE Bacterial polypeptide #4114.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 8; Length 311;
Pred. No. 26;
RESULT 468
ID ADS28526 standard; protein; 399 AA.
DE Bacterial polypeptide #17559.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 8; Length 399;
Pred. No. 37;
RESULT 469
ID ADH8873 standard; protein; 426 AA.
DE Enterococcus faecalis polypeptide #3353.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 7; Length 426;
Pred. No. 40;
RESULT 470
ID ADN22687 standard; protein; 455 AA.
DE Bacterial polypeptide #5340.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 8; Length 455;
Pred. No. 44;
RESULT 471
ID AAY56637 standard; protein; 490 AA.
DE hCAT binding human antibody molecule protein sequence.
PN EP960942-A2.
PD 01-DEC-1999.
PA (INTR-) INTROGENE BV.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 3; Length 490;

Best Local Similarity 25.3%; Pred. No. 49;
RESULT 472
ID ADS28937 standard; protein; 531 AA.
DE Bacterial polypeptide #17970.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 8; Length 531;
Pred. No. 54;
RESULT 473
ID AAY22164 standard; protein; 658 AA.
DE Human TIGIR protein sequence.
PN WO9919480-A2.
PD 01-JUL-1999.
PA (IMMV) IMMUNEX CORP.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 2; Length 658;
Pred. No. 73;
RESULT 474
ID AAY14128 standard; protein; 686 AA.
DE Human IL-1RD8 protein sequence.
PN WO9919480-A2.
PD 22-APR-1999.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 2; Length 686;
Pred. No. 77;
RESULT 475
ID AAF16567 standard; protein; 686 AA.
DE Human interleukin-1 receptor DNX designation 8 (IL-1RD8) protein #2.
PN US6326472-B1.
PD 04-DEC-2001.
PA (SCHE) SCHERING CORP.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 5; Length 686;
Pred. No. 77;
RESULT 476
ID ABP43986 standard; protein; 686 AA.
DE Receptor 9 (IL1R9).
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSER INC.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 5; Length 686;
Pred. No. 77;
RESULT 477
ID ADB31955 standard; protein; 686 AA.
DE Human interleukin-1 receptor DNX designation 8 (IL-1RD8) #2.
PN US2003055218-A1.
PD 20-MAR-2003.
PA (TIMA/) TIMANS J C.
PA (DEBE/) ANTONIUS DEBETS J E M.
PA (SANA/) SANTA T R.
PA (BAZA/) BAZAN J F.
PA (KAST/) KASTELBORN R A.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 7; Length 686;
Pred. No. 77;
RESULT 478
ID ABO85020 standard; protein; 736 AA.
DE Murine cancer-associated protein (CAP) MP07-113.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 8; Length 736;
Pred. No. 85;
RESULT 479
ID ABB48686 standard; protein; 1036 AA.
DE Listeria monocytogenes protein #1390.
PN WO200177315-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 6.2%; Score 74.5; DB 5; Length 1036;
Pred. No. 1.4e+02;

RESULT 480
ID ABB61693 standard; protein; 1511 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11871.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 74.5; DB 4; Length 1511;
Best Local Similarity 25.9%; Pred. No. 2.3e+02;
RESULT 481
ID ADR90278 standard; peptide; 21 AA.
DE Rice intracellular transport/FliI-related Hda peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 6.1%; Score 74; DB 8; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.74;
RESULT 482
ID AAR30777 standard; protein; 233 AA.
DE pH2-9.0 humanised murine anti-CD18 antibody light chain.
PN WO9222653-A1.
PD 23-DEC-1992.
PA (GERTH) GENEWTECH INC.
Query Match 6.1%; Score 74; DB 2; Length 233;
Best Local Similarity 23.4%; Pred. No. 20;
RESULT 483
ID ABB49425 standard; protein; 319 AA.
DE Listeria monocytogenes protein #2129.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.1%; Score 74; DB 5; Length 319;
Best Local Similarity 36.8%; Pred. No. 31;
RESULT 484
ID ABB32491 standard; protein; 319 AA.
DE Protein encoded by Prokaryotic essential gene #18018.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 74; DB 6; Length 319;
Best Local Similarity 36.8%; Pred. No. 31;
RESULT 485
ID AAW92278 standard; protein; 339 AA.
DE Human digestive system antigen SEQ ID NO: 1627.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 74; DB 4; Length 339;
Best Local Similarity 22.4%; Pred. No. 33;
RESULT 486
ID ADI17327 standard; protein; 504 AA.
DE Polypeptide homologous to a human NOVX domain Segid 863.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CGRU-) CTRAGEN CORP.
Query Match 6.1%; Score 74; DB 5; Length 504;
Best Local Similarity 23.0%; Pred. No. 58;
RESULT 487
ID AAY06927 standard; protein; 548 AA.
DE C. albicans antigenic protein 3.
PN WO9916881-A1.
PD 08-APR-1999.
PA (TAKI) TAKARA SHUZO CO LTD.
Query Match 6.1%; Score 74; DB 2; Length 548;
Best Local Similarity 26.5%; Pred. No. 65;
RESULT 488
ID ABB93338 standard; protein; 548 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 674.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.1%; Score 74; DB 5; Length 548;
Best Local Similarity 26.5%; Pred. No. 65;
RESULT 489

ID ABB93361 standard; protein; 548 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 480.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.1%; Score 74; DB 5; Length 548;
Best Local Similarity 26.5%; Pred. No. 65;
RESULT 490
ID AAE25098 standard; protein; 2038 AA.
DE Human kinase and phosphatase-18 (KAP-18) protein.
PN WO200246384-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 74; DB 5; Length 2038;
Best Local Similarity 24.5%; Pred. No. 3.9e+02;
RESULT 491
ID ABB78990 standard; protein; 2092 AA.
DE Modifier of beta-catenin (MBCAT) polypeptide GI 27498257.
PN WO2003074725-A2.
PD 12-SEP-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 6.1%; Score 74; DB 7; Length 2092;
Best Local Similarity 24.5%; Pred. No. 4.1e+02;
RESULT 492
ID ABB70161 standard; protein; 2092 AA.
DE Human heat mitochondrial protein as a therapeutic target Segid1967.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 6.1%; Score 74; DB 7; Length 2092;
Best Local Similarity 24.5%; Pred. No. 4.1e+02;
RESULT 493
ID ABB13933 standard; protein; 2247 AA.
DE Human endometrial-specific protein - SEQ ID 564.
PN WO2003059927-A1.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.1%; Score 74; DB 7; Length 2247;
Best Local Similarity 24.5%; Pred. No. 4.5e+02;
RESULT 494
ID ABB13934 standard; protein; 2383 AA.
DE Human endometrial-specific protein - SEQ ID 565.
PN WO2003059927-A1.
PD 24-JUL-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.1%; Score 74; DB 7; Length 2383;
Best Local Similarity 24.5%; Pred. No. 4.8e+02;
RESULT 495
ID AAE21713 standard; protein; 2429 AA.
DE Human PKIN-8 protein.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 74; DB 5; Length 2429;
Best Local Similarity 24.5%; Pred. No. 5e+02;
RESULT 496
ID ABB78989 standard; protein; 2429 AA.
DE Modifier of beta-catenin (MBCAT) polypeptide GI 18561840.
PN WO2003074725-A2.
PD 12-SEP-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 6.1%; Score 74; DB 7; Length 2429;
Best Local Similarity 24.5%; Pred. No. 5e+02;
RESULT 497
ID ABB35146 standard; protein; 244 AA.
DE Actinobacter baumannii protein #2307.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73.5; DB 6; Length 244;
Best Local Similarity 24.3%; Pred. No. 24;
RESULT 498

ID AD542454 standard; protein: 287 AA.
DE Bacterial polypeptide #20884.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 8; Length 287;
Best Local Similarity 23.2%; Pred. No. 30;
RESULT 499
ID AD16909 standard; protein: 429 AA.
DE Human NOVX protein homologue SeqID 445.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 5; Length 429;
Best Local Similarity 22.6%; Pred. No. 53;
RESULT 500
ID AAW4909 standard; protein: 503 AA.
DE Signal regulatory protein 4 (SIRP4).
PN WO9748723-A2.
PD 24-DEC-1997.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 2; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 501
ID AAW40481 standard; protein: 503 AA.
DE Human SH2 binding protein.
PN JP10084972-A.
PD 07-APR-1998.
PA (KIRI) KIRIN BREWERY KK.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 2; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 502
ID AAU79036 standard; protein: 503 AA.
DE Human SHPS-1 (not defined) receptor.
PN WO200218938-A1.
PD 07-MAR-2002.
PA (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 5; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 503
ID AD16906 standard; protein: 503 AA.
DE Human NOVX protein homologue SeqID 442.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 5; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 504
ID ABU89765 standard; protein: 503 AA.
DE Protein differentially expressed in cardiovascular disease #59.
PN WO2003031650-A2.
PD 17-APR-2003.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 6; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 505
ID ADE56369 standard; protein: 503 AA.
DE Human Protein NP_004639, SEQ ID NO 2221.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 7; Length 503;
Best Local Similarity 22.6%; Pred. No. 65;
RESULT 506
ID AD16905 standard; protein: 504 AA.
DE Human NOVX protein homologue SeqID 441.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 5; Length 504;
Best Local Similarity 22.6%; Pred. No. 66;
RESULT 507
ID ADD5286 standard; protein: 504 AA.
DE Human Protein DB6043, SEQ ID NO 10719.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 7; Length 504;
Best Local Similarity 22.6%; Pred. No. 66;
RESULT 508
ID AD770379 standard; protein: 504 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2185.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 7; Length 504;
Best Local Similarity 22.6%; Pred. No. 66;
RESULT 509
ID ADM67213 standard; protein: 504 AA.
DE Human homologue of murine adipocyte specific BIT protein SeqID 567.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 8; Length 504;
Best Local Similarity 22.6%; Pred. No. 66;
RESULT 510
ID AD183046 standard; protein: 504 AA.
DE Human PR084698, SEQ ID 248.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 8; Length 504;
Best Local Similarity 22.6%; Pred. No. 66;
RESULT 511
ID ABB58921 standard; protein: 558 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3555.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 4; Length 558;
Best Local Similarity 22.5%; Pred. No. 75;
RESULT 512
ID ABB58920 standard; protein: 693 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 4; Length 693;
Best Local Similarity 22.5%; Pred. No. 1e+02;
RESULT 513
ID ABG06343 standard; protein: 816 AA.
DE Novel human diagnostic protein #6334.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 4; Length 816;
Best Local Similarity 22.6%; Pred. No. 1.3e+02;
RESULT 514
ID ADB09996 standard; protein: 816 AA.
DE Novel protein-related contig polypeptide sequence #584.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73.5; DB 7; Length 816;
Best Local Similarity 22.6%; Pred. No. 1.3e+02;
RESULT 515
ID ABW83619 standard; protein: 845 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3868.
PN WO2004023973-A2.

PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.1%; Score 73.5; DB 8; Length 845;
Best Local Similarity 19.4%; Pred. No. 1.3e+02;
RESULT 516
ID ABM85719 standard; protein; 1102 AA.
DE Human protein sequence hCP33890.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.1%; Score 73.5; DB 7; Length 1102;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 517
ID ADQ39233 standard; protein; 1102 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 896.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.1%; Score 73.5; DB 8; Length 1102;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 518
ID ADQ39232 standard; protein; 1102 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 895.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.1%; Score 73.5; DB 8; Length 1102;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 519
ID ADK40897 standard; protein; 1103 AA.
DE Novel human kinase protein #4.
PD 17-JUL-2003.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Query Match 6.1%; Score 73.5; DB 7; Length 1103;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 520
ID ADRI5621 standard; protein; 1103 AA.
DE Kinase 33890 hCT7976 1, SEQ ID 14.
PD 19-AUG-2004.
PA (GRIG/) GRIGORIEV I V.
PA (SUDA/) SUDARSANAM S.
Query Match 6.1%; Score 73.5; DB 8; Length 1103;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 521
ID ABJ38696 standard; protein; 1388 AA.
DE Human nucleic acid-associated protein (NAAP) #26.
PD 06-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 73.5; DB 6; Length 1388;
Best Local Similarity 23.1%; Pred. No. 2.6e+02;
RESULT 522
ID ADJ6933 standard; protein; 1388 AA.
DE Human heart mitochondrial protein as a therapeutic target SegID1139.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INSTR AGE RES.
Query Match 6.1%; Score 73.5; DB 7; Length 1388;
Best Local Similarity 23.1%; Pred. No. 2.6e+02;
RESULT 523
ID ADN90277 standard; peptide; 21 AA.
DE Salsuna orange intracellular transport/TFII-related ClFT peptide.
PD 24-SEP-2004.
PA (DOKU-) DOXURITSU GYOSHI HOJIN KAGAKU GIUTSU SH.
Query Match 6.1%; Score 73; DB 8; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.95;
RESULT 524
ID ADN20201 standard; protein; 314 AA.

DE Bacterial polypeptide #2854.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 73; DB 8; Length 314;
Best Local Similarity 29.1%; Pred. No. 39;
RESULT 525
ID AAY81990 standard; protein; 458 AA.
DE Chimeric PCB decomposing enzyme protein #2.
PD 07-MAR-2000.
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 6.1%; Score 73; DB 3; Length 458;
Best Local Similarity 24.9%; Pred. No. 66;
RESULT 526
ID ADC51244 standard; protein; 458 AA.
DE P. pseudocalligenes biphenyl dioxygenase (BphA1) protein.
PD 07-JAN-2003.
PA (KIRI) KIRIN BREWERY KK.
Query Match 6.1%; Score 73; DB 7; Length 458;
Best Local Similarity 24.9%; Pred. No. 66;
RESULT 527
ID ADC51236 standard; protein; 458 AA.
DE P. pseudocalligenes aromatic ring dioxygenase containing alpha subunit.
PD 07-JAN-2003.
PA (KIRI) KIRIN BREWERY KK.
Query Match 6.1%; Score 73; DB 7; Length 458;
Best Local Similarity 24.9%; Pred. No. 66;
RESULT 528
ID ADR09326 standard; protein; 496 AA.
DE Human protein useful for treating neurological disease Seq 2832.
PD 18-AUG-2004.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 73; DB 8; Length 496;
Best Local Similarity 22.3%; Pred. No. 73;
RESULT 529
ID ABJ25939 standard; protein; 508 AA.
DE Aspergillus fumigatus essential gene protein #597.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 508;
Best Local Similarity 27.6%; Pred. No. 76;
RESULT 530
ID ABJ25642 standard; protein; 508 AA.
DE Aspergillus fumigatus essential gene protein #500.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 508;
Best Local Similarity 27.6%; Pred. No. 76;
RESULT 531
ID ADM26102 standard; protein; 585 AA.
DE Hyperthermophile Methanopyrus kandleri protein #708.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALV/) MALVYR A.
Query Match 6.1%; Score 73; DB 7; Length 585;
Best Local Similarity 28.1%; Pred. No. 92;
RESULT 532
ID AAO16436 standard; protein; 602 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID No 33.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 6.1%; Score 73; DB 6; Length 602;
Best Local Similarity 22.3%; Pred. No. 95;
RESULT 533
ID ADP87635 standard; protein; 654 AA.
DE Human NOVX polypeptide, NOV11h.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 654;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 534
ID ADP87627 standard; protein; 654 AA.
DE Human NOVX polypeptide, NOV11d.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 654;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 535
ID ADP87637 standard; protein; 660 AA.
DE Human NOVX polypeptide, NOV11i.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 660;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 536
ID ADP87631 standard; protein; 660 AA.
DE Human NOVX polypeptide, NOV11f.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 660;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 537
ID ADP87629 standard; protein; 661 AA.
DE Human NOVX polypeptide, NOV11e.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 661;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 538
ID ADP87633 standard; protein; 661 AA.
DE Human NOVX polypeptide, NOV11g.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 661;
Best Local Similarity 27.6%; Pred. No. 1.1e+02;
RESULT 539
ID ADP87732 standard; protein; 747 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID538.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.1%; Score 73; DB 7; Length 747;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 540
ID ADM32868 standard; protein; 747 AA.
DE Protein sequence of a human adenosine monophosphate deaminase (AMPD).
PN WO2004024880-A2.
PD 25-MAR-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 6.1%; Score 73; DB 8; Length 747;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 541
ID ADQ18475 standard; protein; 747 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1294.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 6.1%; Score 73; DB 8; Length 747;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 542
ID ADP87621 standard; protein; 747 AA.
DE Human NOVX polypeptide, NOV11a.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 747;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 543
ID ADP87625 standard; protein; 748 AA.
DE Human NOVX polypeptide, NOV11c.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 748;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 544
ID ADP87623 standard; protein; 751 AA.
DE Human NOVX polypeptide, NOV11b.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 751;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 545
ID ABO85021 standard; protein; 758 AA.
DE Human cancer-associated protein (CAP) HP07-113.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.1%; Score 73; DB 8; Length 758;
Best Local Similarity 27.6%; Pred. No. 1.3e+02;
RESULT 546
ID AAW70506 standard; protein; 1711 AA.
DE Osteoclastic protein tyrosine phosphatase protein.
PN US5821084-A.
PD 13-OCT-1998.
PA (UNMI) UNIV MICHIGAN.
PA (AMHP) AMERICAN HOME PROD CORP.
Query Match 6.1%; Score 73; DB 2; Length 1711;
Best Local Similarity 21.9%; Pred. No. 4e+02;
RESULT 547
ID AAW70507 standard; protein; 1711 AA.
DE Mutant osteoclastic protein tyrosine phosphatase protein.
PN US5821084-A.
PD 13-OCT-1998.
PA (UNMI) UNIV MICHIGAN.
PA (AMHP) AMERICAN HOME PROD CORP.
Query Match 6.1%; Score 73; DB 2; Length 1711;
Best Local Similarity 21.9%; Pred. No. 4e+02;
RESULT 548
ID ABR52349 standard; protein; 1711 AA.
DE Protein relating to the invention SEQ ID NO: 38.
PN WO200257460-A2.
PD 25-JUL-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.1%; Score 73; DB 5; Length 1711;
Best Local Similarity 21.9%; Pred. No. 4e+02;
RESULT 549
ID ABG02232 standard; protein; 1813 AA.
DE Novel human diagnostic protein #223.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 1813;
Best Local Similarity 27.6%; Pred. No. 4.3e+02;
RESULT 550
ID ABJ34042 standard; protein; 214 AA.
DE Protein encoded by Prokaryotic essential gene #19569.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (BLIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72.5; DB 6; Length 214;
Best Local Similarity 25.5%; Pred. No. 26;
RESULT 551
ID AAY83092 standard; protein; 327 AA.
DE F-box protein FBP-24.
PN WO20012679-A1.
PD 09-MAR-2000.
PA (UNYV) UNIV NEW YORK STATE.
Query Match 6.0%; Score 72.5; DB 3; Length 327;
Best Local Similarity 23.4%; Pred. No. 47;
RESULT 552
ID AAB35162 standard; protein; 327 AA.
DE Human Skp1-associated F-box protein-2 SAF-2 SEQ ID NO: 12.
PN WO20007207-A2.
PD 21-DEC-2000.
PA (BURN-) BURNHAM INST.
Query Match 6.0%; Score 72.5; DB 4; Length 327;
Best Local Similarity 23.4%; Pred. No. 47;
RESULT 553
ID AAO2478 standard; protein; 327 AA.
DE Human F-box protein FBP24 SEQ ID NO 58.
PN WO200255665-A2.
PD 18-JUL-2002.
PA (UNYV) UNIV NEW YORK STATE.
Query Match 6.0%; Score 72.5; DB 5; Length 327;
Best Local Similarity 23.4%; Pred. No. 47;
RESULT 554
ID ABA41675 standard; protein; 379 AA.
DE Human ovarian antigen HSDUR27, SEQ ID NO:2807.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72.5; DB 5; Length 379;
Best Local Similarity 23.4%; Pred. No. 58;
RESULT 555
ID AAM39753 standard; protein; 405 AA.
DE Human polypeptide SEQ ID NO 2898.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72.5; DB 4; Length 405;
Best Local Similarity 23.4%; Pred. No. 63;
RESULT 556
ID ABB89459 standard; protein; 408 AA.
DE Human polypeptide SEQ ID NO 1835.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72.5; DB 5; Length 408;
Best Local Similarity 23.4%; Pred. No. 64;
RESULT 557
ID AAM41539 standard; protein; 430 AA.
DE Human polypeptide SEQ ID NO 6470.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72.5; DB 4; Length 430;
Best Local Similarity 23.4%; Pred. No. 68;
RESULT 558
ID AAB93745 standard; protein; 437 AA.
DE Human protein sequence SEQ ID NO:13403.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.0%; Score 72.5; DB 4; Length 437;
Best Local Similarity 23.4%; Pred. No. 70;
RESULT 559
ID AAD71063 standard; protein; 731 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID2869.
PN WO200308768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 6.0%; Score 72.5; DB 7; Length 731;
Best Local Similarity 21.5%; Pred. No. 1.4e+02;
RESULT 560
ID ABB20820 standard; protein; 1009 AA.
DE Novel human diagnostic protein #20811.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72.5; DB 4; Length 1009;
Best Local Similarity 20.6%; Pred. No. 2.2e+02;
RESULT 561
ID ADP30309 standard; protein; 1047 AA.
DE Human secreted protein SEQ ID #1076.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.0%; Score 72.5; DB 8; Length 1047;
Best Local Similarity 20.6%; Pred. No. 2.3e+02;
RESULT 562
ID AAM23948 standard; protein; 1102 AA.
DE Porcine phosphoinositide 3OH-kinase p120 subunit.
PN WO9749818-A2.
PD 31-DEC-1997.
PA (ONYX-) ONYX PHARM.
Query Match 6.0%; Score 72.5; DB 2; Length 1102;
Best Local Similarity 20.5%; Pred. No. 2.5e+02;
RESULT 563
ID AAM90083 standard; protein; 1102 AA.
DE Porcine G-protein regulated PI3K p120 adapter subunit protein.
PN US5856132-A.
PD 05-JAN-1999.
PA (ONYX-) ONYX PHARM.
Query Match 6.0%; Score 72.5; DB 2; Length 1102;
Best Local Similarity 20.5%; Pred. No. 2.5e+02;
RESULT 564
ID AAY76802 standard; protein; 1102 AA.
DE Pig p120 regulatory subunit proteinsequence.
PN US6017763-A.
PD 25-JAN-2000.
PA (ONYX-) ONYX PHARM INC.
Query Match 6.0%; Score 72.5; DB 3; Length 1102;
Best Local Similarity 20.5%; Pred. No. 2.5e+02;
RESULT 565
ID ABB09753 standard; protein; 1102 AA.
DE Human phosphoinositide 3-Kinase gamma (PI3Kgamma).
PN US2003022344-A1.
PD 30-JAN-2003.
PA (WILL/) WILLIAMS R.
PA (RIED/) RIED C.
PA (WALK/) WALKER E H.
PA (STEP/) STEPHENS L.
Query Match 6.0%; Score 72.5; DB 6; Length 1102;
Best Local Similarity 20.5%; Pred. No. 2.5e+02;
RESULT 566
ID AAY23899 standard; protein; 1192 AA.
DE Human reseinlin binding armadillo protein p0071.
PN WO9935501-A1.
PD 15-JUL-1999.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
Query Match 6.0%; Score 72.5; DB 2; Length 1192;
Best Local Similarity 20.6%; Pred. No. 2.8e+02;
RESULT 567
ID AAM24560 standard; protein; 1211 AA.
DE Presentilin-interacting protein p0071.
PN WO9727296-A1.
PD 31-JUL-1997.
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
Query Match 6.0%; Score 72.5; DB 2; Length 1211;
Best Local Similarity 20.6%; Pred. No. 2.8e+02;
RESULT 568

ID AA92336 standard; protein; 1211 AA.
DE Human P0071.
PN WO200020448-A2.
PD 13-APR-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 72.5; DB 3; Length 1211;
Best Local Similarity 20.6%; Pred. No. 2.8e+02;
RESULT 569
ID ABB79001 standard; protein; 1211 AA.
DE Human P0071 protein sequence SEQ ID NO:4487.
PN WO200229086-A2.
PD 11-APR-2002.
PA (FAR) BAYER CORP.
Query Match 6.0%; Score 72.5; DB 5; Length 1211;
Best Local Similarity 20.6%; Pred. No. 2.8e+02;
RESULT 570
ID ABB61674 standard; protein; 2727 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11814.
PN WO20011042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 6.0%; Score 72.5; DB 4; Length 2727;
Best Local Similarity 21.0%; Pred. No. 8.6e+02;
RESULT 571
ID ADR90279 standard; peptide; 21 AA.
DE Rice Intracellular transport/TPL1-related RPT1 peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIYUTSU SH.
Query Match 6.0%; Score 72; DB 8; Length 21;
Best Local Similarity 61.9%; Pred. No. 1.2;
RESULT 572
ID ABB08420 standard; protein; 84 AA.
DE Human ORFX protein sequence SEQ ID NO:16822.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 72; DB 5; Length 84;
Best Local Similarity 28.4%; Pred. No. 8.3;
RESULT 573
ID ABR41599 standard; protein; 252 AA.
DE Human DITP antigen recognition protein.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 72; DB 6; Length 252;
Best Local Similarity 22.8%; Pred. No. 38;
RESULT 574
ID ABB07796 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #13323.
PN WO20027163-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 275;
Best Local Similarity 23.2%; Pred. No. 42;
RESULT 575
ID AD990726 standard; protein; 276 AA.
DE Synchocystis sp. carboxylesterase protein SEQ ID NO:2.
PN WO2003072792-A2.
PD 04-SEP-2003.
PA (SYGN) SYNGENTA LTD.
Query Match 6.0%; Score 72; DB 7; Length 276;
Best Local Similarity 28.8%; Pred. No. 42;
RESULT 576
ID ABO59304 standard; protein; 379 AA.
DE Human genome derived single exon protein #5538.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENNY) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.0%; Score 72; DB 8; Length 379;
Best Local Similarity 18.9%; Pred. No. 66;

RESULT 577
ID ABO73412 standard; protein; 396 AA.
DE Pseudomonas aeruginosa polypeptide #5587.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 72; DB 7; Length 396;
Best Local Similarity 26.8%; Pred. No. 70;
RESULT 578
ID AAG41753 standard; protein; 463 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51987.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 463;
Best Local Similarity 24.7%; Pred. No. 86;
RESULT 579
ID AAG41752 standard; protein; 493 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51986.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 493;
Best Local Similarity 24.7%; Pred. No. 94;
RESULT 580
ID AAG41751 standard; protein; 600 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51985.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 600;
Best Local Similarity 24.7%; Pred. No. 1.2e+02;
RESULT 581
ID AAY52700 standard; protein; 633 AA.
DE Pleurotus cornucopiae antitumour protein.
PN JP11315096-A.
PD 16-NOV-1999.
PA (NEMF-) NEW FOOD CREATION GIYUTSU KENKYU KUMAI.
Query Match 6.0%; Score 72; DB 3; Length 633;
Best Local Similarity 22.3%; Pred. No. 1.3e+02;
RESULT 582
ID ADS29632 standard; protein; 651 AA.
DE Bacterial polypeptide #18865.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CNOY/) CNO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 72; DB 8; Length 651;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 583
ID ABR53095 standard; protein; 1104 AA.
DE Protein sequence #SEQ ID 1055.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 72; DB 6; Length 1104;
Best Local Similarity 22.1%; Pred. No. 2.8e+02;
RESULT 584
ID ADK63000 standard; protein; 1104 AA.
DE Disease treating protein complex-derived protein #626.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 72; DB 7; Length 1104;
Best Local Similarity 22.1%; Pred. No. 2.8e+02;
RESULT 585
ID ABB97332 standard; protein; 1554 AA.
DE Novel human protein SEQ ID NO: 600.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72; DB 5; Length 1554;
Best Local Similarity 20.9%; Pred. No. 4.5e+02;

RESULT 586
ID ABB70137 standard; protein; 1908 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37203.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.0%; Score 72; DB 4; Length 1908;
Pred. No. 6e+02;
RESULT 587
ID ABB06540 standard; protein; 113 AA.
DE Human ORFX protein sequence SEQ ID NO:13062.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 5; Length 113;
Pred. No. 14;
RESULT 588
ID ABB70680 standard; protein; 184 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38832.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 4; Length 184;
Pred. No. 28;
RESULT 589
ID AAG57785 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74507.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 235;
Pred. No. 39;
RESULT 590
ID AAG57786 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74509.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 235;
Pred. No. 39;
RESULT 591
ID AAG55516 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 71200.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 235;
Pred. No. 39;
RESULT 592
ID AAG57791 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74515.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 235;
Pred. No. 39;
RESULT 593
ID AAG55515 standard; protein; 302 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 71199.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 302;
Pred. No. 55;
RESULT 594
ID AAG57790 standard; protein; 408 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74514.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 408;
Pred. No. 83;
RESULT 595
ID AAG57789 standard; protein; 413 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74513.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 413;
Pred. No. 84;

RESULT 596
ID AAM19735 standard; protein; 421 AA.
DE Sugar biosynthesis enzyme EryCIII.
PN WO9723630-A2.
PD 03-JUL-1997.
PA (ABBOTT) ABBOTT LAB.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 2; Length 421;
Pred. No. 86;
RESULT 597
ID AAM99388 standard; protein; 421 AA.
DE S. erythraea deoxyaminyltransferase.
PN WO9905283-A2.
PD 04-FEB-1999.
PA (HMRI) HOECHST MARION ROUSSEL.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 2; Length 421;
Pred. No. 86;
RESULT 598
ID AAY9615 standard; protein; 422 AA.
DE A. thaliana Vb3 CDC2b interacting protein.
PN WO200036124-A2.
PD 22-JUN-2000.
PA (CROP-) CROPDISEIGN NV.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 422;
Pred. No. 87;
RESULT 599
ID AAG59392 standard; protein; 455 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76819.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 455;
Pred. No. 96;
RESULT 600
ID AAG59391 standard; protein; 486 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76818.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 486;
Pred. No. 1.1e+02;
RESULT 601
ID ABU07707 standard; protein; 511 AA.
DE Human ankyrin-56.21-protein.
PN CN1376687-A.
PD 30-OCT-2002.
PA (BIOW-) BIOWINDOM GENE DEV INC SHANGHAI.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 6; Length 511;
Pred. No. 1.1e+02;
RESULT 602
ID AAG59390 standard; protein; 530 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76817.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 3; Length 530;
Pred. No. 1.2e+02;
RESULT 603
ID ABG00470 standard; protein; 560 AA.
DE Novel human diagnostic protein #461.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 4; Length 560;
Pred. No. 1.3e+02;
RESULT 604
ID AAM58956 standard; protein; 575 AA.
DE C. acidivorans gamma-lactamase protein.
PN WO9810075-A1.
PD 12-MAR-1998.
PA (CHIR-) CHIROSCIENCE LTD.
Query Match
Best Local Similarity 5.9%; Score 71.5; DB 2; Length 575;
Pred. No. 1.3e+02;
RESULT 605
ID ADN19428 standard; protein; 712 AA.
DE Bacterial polypeptide #2081.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 71.5; DB 8; Length 712;
Best Local Similarity 20.1%; Pred. No. 1.8e+02;
RESULT 606
ID AAY38834 standard; protein; 725 AA.
DE Neisseria gonorrhoeae antigenic protein encoded by ORF23.
PN WO924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 71.5; DB 2; Length 725;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 607
ID AAY38832 standard; protein; 725 AA.
DE Neisseria meningitidis strain A antigen encoded by ORF23.
PN WO924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 71.5; DB 2; Length 725;
Best Local Similarity 21.7%; Pred. No. 1.8e+02;
RESULT 608
ID ABP77503 standard; protein; 725 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 1536.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 71.5; DB 6; Length 725;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 609
ID ABU37822 standard; protein; 725 AA.
DE Protein encoded by Prokaryotic essential gene #23349.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71.5; DB 6; Length 725;
Best Local Similarity 21.7%; Pred. No. 1.8e+02;
RESULT 610
ID ABU37447 standard; protein; 725 AA.
DE Protein encoded by Prokaryotic essential gene #22974.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71.5; DB 6; Length 725;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 611
ID ABG70650 standard; protein; 747 AA.
DE Rabbit adenosine monophosphate deaminase (AMPA).
PN EP1215587-A2.
PD 19-JUN-2002.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 5.9%; Score 71.5; DB 5; Length 747;
Best Local Similarity 27.8%; Pred. No. 1.9e+02;
RESULT 612
ID AAU29336 standard; protein; 774 AA.
DE Novel mar regulated protein (NIMR) #8.
PN WO200170776-A2.
PD 27-SEP-2001.
PA (TUFT) TUFTS COLLEGE.
Query Match 5.9%; Score 71.5; DB 4; Length 774;
Best Local Similarity 22.2%; Pred. No. 2e+02;
RESULT 613
ID ABU15308 standard; protein; 774 AA.
DE Protein encoded by Prokaryotic essential gene #835.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71.5; DB 6; Length 774;
Best Local Similarity 22.2%; Pred. No. 2e+02;

RESULT 614
ID ADX13830 standard; protein; 774 AA.
DE E. coli iron transport and metabolism protein SEQ ID NO.125.
PN WO2004018638-A2.
PD 04-MAR-2004.
PA (MTNU) UNITV MINNESOTA.
PA (KAPU/) KAPUR V.
PA (GADG/) GADGIL M.
Query Match 5.9%; Score 71.5; DB 8; Length 774;
Best Local Similarity 22.2%; Pred. No. 2e+02;
RESULT 615
ID ABG03507 standard; protein; 816 AA.
DE Novel human diagnostic protein #3498.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 71.5; DB 4; Length 816;
Best Local Similarity 20.1%; Pred. No. 2.1e+02;
RESULT 616
ID ABG20940 standard; protein; 861 AA.
DE Novel human diagnostic protein #20931.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 71.5; DB 4; Length 861;
Best Local Similarity 26.4%; Pred. No. 2.3e+02;
RESULT 617
ID ADS30067 standard; protein; 1005 AA.
DE Bacterial polypeptide #19100.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 71.5; DB 8; Length 1005;
Best Local Similarity 23.6%; Pred. No. 2.9e+02;
RESULT 618
ID ADR90280 standard; peptide; 21 AA.
DE Rice intracellular transport/TFII-related AL662946 peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.9%; Score 71; DB 8; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.6;
RESULT 619
ID ABW73218 standard; protein; 171 AA.
DE Staphylococcus aureus protein #2458.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 71; DB 6; Length 171;
Best Local Similarity 26.2%; Pred. No. 29;
RESULT 620
ID ADH86948 standard; protein; 190 AA.
DE Enterococcus faecalis polypeptide #1428.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.9%; Score 71; DB 7; Length 190;
Best Local Similarity 20.1%; Pred. No. 33;
RESULT 621
ID ABG99173 standard; protein; 283 AA.
DE Human endogenous retrovirus k10 (herv-k10) gag #1.
PN WO200246477-A2.
PD 13-JUN-2002.
PA (CHIR) CHIRON CORP.
Query Match 5.9%; Score 71; DB 5; Length 283;
Best Local Similarity 27.3%; Pred. No. 57;
RESULT 622
ID ADU83831 standard; protein; 283 AA.

DE HERV-K HML-2 subgroup HERV-K10 gag protein 1.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR) CHIRON CORP.
Query Match 5.9%; Score 71; DB 8; Length 283;
Best Local Similarity 27.3%; Pred. No. 57;
RESULT 623
ID ABG14883 standard; protein; 316 AA.
DE Novel human diagnostic protein #14874.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 71; DB 4; Length 316;
Best Local Similarity 23.1%; Pred. No. 66;
RESULT 624
ID ABH29132 standard; protein; 316 AA.
DE Protein encoded by Prokaryotic essential gene #14659.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 316;
Best Local Similarity 20.1%; Pred. No. 66;
RESULT 625
ID AB061502 standard; protein; 389 AA.
DE Klebsiella pneumoniae polypeptide seqid 8019.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 71; DB 7; Length 389;
Best Local Similarity 23.5%; Pred. No. 88;
RESULT 626
ID AD066654 standard; protein; 577 AA.
DE Novel human protein sequence #1627.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (RAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 71; DB 8; Length 577;
Best Local Similarity 23.6%; Pred. No. 1.5e+02;
RESULT 627
ID ABH30576 standard; protein; 659 AA.
DE Protein encoded by Prokaryotic essential gene #16103.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 659;
Best Local Similarity 24.0%; Pred. No. 1.8e+02;
RESULT 628
ID ABG10523 standard; protein; 755 AA.
DE Novel human diagnostic protein #10514.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 71; DB 4; Length 755;
Best Local Similarity 29.1%; Pred. No. 2.2e+02;
RESULT 629
ID AB071485 standard; protein; 757 AA.
DE Pseudomonas aeruginosa polypeptide #3660.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 71; DB 7; Length 757;
Best Local Similarity 24.8%; Pred. No. 2.2e+02;
RESULT 630
ID AAB23271 standard; protein; 860 AA.
DE Balaanus amphitrite adhesion/metamorphosis-related protein Bcs-5.
PN JP2000228985-A.
PD 22-AUG-2000.
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
Query Match 5.9%; Score 71; DB 3; Length 860;
Best Local Similarity 20.0%; Pred. No. 2.6e+02;
RESULT 631
ID ABG10524 standard; protein; 930 AA.
DE Novel human diagnostic protein #10515.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 71; DB 4; Length 930;
Best Local Similarity 29.1%; Pred. No. 2.9e+02;
RESULT 632
ID ADD14037 standard; protein; 1498 AA.
DE Human src biomarker polypeptide SEQ ID NO:226.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.9%; Score 71; DB 7; Length 1498;
Best Local Similarity 21.0%; Pred. No. 5.6e+02;
RESULT 633
ID AD019580 standard; protein; 1498 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2399.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 71; DB 8; Length 1498;
Best Local Similarity 21.0%; Pred. No. 5.6e+02;
RESULT 634
ID AAB36107 standard; protein; 1944 AA.
DE Human chromodomain helicase DNA binding protein (CHD) #5.
PN WO200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.9%; Score 71; DB 6; Length 1944;
Best Local Similarity 23.6%; Pred. No. 8e+02;
RESULT 635
ID AD126773 standard; protein; 1944 AA.
DE Human CHD3, SEQ ID 30.
PN FR2837391-A1.
PD 26-SEP-2003.
PA (GENE-) GENE SIGNAL.
Query Match 5.9%; Score 71; DB 7; Length 1944;
Best Local Similarity 23.6%; Pred. No. 8e+02;
RESULT 636
ID AD126772 standard; protein; 1944 AA.
DE Human CHD3, SEQ ID 29.
PN FR2837391-A1.
PD 26-SEP-2003.
PA (GENE-) GENE SIGNAL.
Query Match 5.9%; Score 71; DB 7; Length 1944;
Best Local Similarity 23.6%; Pred. No. 8e+02;
RESULT 637
ID ADJ68739 standard; protein; 1944 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID545.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 5.9%; Score 71; DB 7; Length 1944;
Best Local Similarity 23.6%; Pred. No. 8e+02;
RESULT 638
ID AD126747 standard; protein; 2000 AA.
DE Human GS-P3 protein, SEQ ID 8.
PN FR2837391-A1.
PD 26-SEP-2003.
PA (GENE-) GENE SIGNAL.
Query Match 5.9%; Score 71; DB 7; Length 2000;
Best Local Similarity 23.6%; Pred. No. 8.4e+02;
RESULT 639
ID ADF60530 standard; protein; 143 AA.
DE Human contig polypeptide sequence SEQ ID NO:2897.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 7; Length 143;
Best Local Similarity 25.2%; Pred. No. 26;

RESULT 640
ID AAO15429 standard; protein; 184 AA.
DE Human TRAF-binding factor protein.
PN WO200257449-A1.
PD 25-JUL-2002.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 5; Length 184;
Best Local Similarity 21.0%; Pred. No. 36;
RESULT 641
ID ABP61464 standard; protein; 184 AA.
DE Human NF-KB activating protein SEQ ID NO 81.
PN WO200253737-A1.
PD 11-JUL-2002.
PA (ASHH) ASAHU KASEI KOGYO KK.
Query Match 5.9%; Score 70.5; DB 5; Length 184;
Best Local Similarity 21.0%; Pred. No. 36;
RESULT 642
ID ABR41029 standard; protein; 184 AA.
DE Human MAP kinase cascade activator #14.
PN WO2003008589-A1.
PD 30-JAN-2003.
PA (ASHH) ASAHU KASEI KOGYO KK.
Query Match 5.9%; Score 70.5; DB 6; Length 184;
Best Local Similarity 21.0%; Pred. No. 36;
RESULT 643
ID ADP36175 standard; protein; 184 AA.
DE Human TRAF2-binding protein amino acid sequence.
PN WO2003082917-A1.
PD 09-OCT-2003.
PA (RIKA) INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 5.9%; Score 70.5; DB 7; Length 184;
Best Local Similarity 21.0%; Pred. No. 36;
RESULT 644
ID ADM90859 standard; protein; 258 AA.
DE Human pharmacologically useful protein SegID 252.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 5.9%; Score 70.5; DB 8; Length 258;
Best Local Similarity 21.7%; Pred. No. 57;
RESULT 645
ID ADM90858 standard; protein; 258 AA.
DE Human pharmacologically useful protein SegID 251.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 5.9%; Score 70.5; DB 8; Length 258;
Best Local Similarity 21.7%; Pred. No. 57;
RESULT 646
ID ABG37323 standard; protein; 368 AA.
DE Novel human diagnostic protein #27314.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 4; Length 368;
Best Local Similarity 26.1%; Pred. No. 93;
RESULT 647
ID AAG04449 standard; protein; 394 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 480.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 394;
Best Local Similarity 15.9%; Pred. No. 1e+02;
RESULT 648
ID ABO61928 standard; protein; 394 AA.
DE Klebsiella pneumoniae polypeptide seqid 8445.
PN US610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 394;
Best Local Similarity 20.1%; Pred. No. 1e+02;
RESULT 649
ID ABB61244 standard; protein; 430 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10524.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 70.5; DB 4; Length 430;
Best Local Similarity 21.0%; Pred. No. 1.2e+02;
RESULT 650
ID AAG04448 standard; protein; 532 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 479.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 532;
Best Local Similarity 15.9%; Pred. No. 1.5e+02;
RESULT 651
ID ADN72639 standard; protein; 532 AA.
DE Thale cress protein upregulated in B2Fa/Dpa expressing plants SegID 534.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPDESIGN NV.
Query Match 5.9%; Score 70.5; DB 8; Length 532;
Best Local Similarity 15.9%; Pred. No. 1.5e+02;
RESULT 652
ID AAG04447 standard; protein; 548 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 478.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 548;
Best Local Similarity 15.9%; Pred. No. 1.6e+02;
RESULT 653
ID ABW70336 standard; protein; 694 AA.
DE Photobabhus luminescens protein sequence #3433.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70.5; DB 6; Length 694;
Best Local Similarity 22.8%; Pred. No. 2.2e+02;
RESULT 654
ID ADN46567 standard; protein; 698 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SegID445.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.9%; Score 70.5; DB 8; Length 698;
Best Local Similarity 21.1%; Pred. No. 2.2e+02;
RESULT 655
ID ADS43712 standard; protein; 830 AA.
DE Bacterial polypeptide #22142.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CMOY/) CMO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 70.5; DB 8; Length 830;
Best Local Similarity 21.4%; Pred. No. 2.8e+02;
RESULT 656
ID ABO81716 standard; protein; 998 AA.
DE Pseudomonas aeruginosa polypeptide #13891.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 998;
Best Local Similarity 23.2%; Pred. No. 3.7e+02;
RESULT 657
ID AAY84034 standard; protein; 1109 AA.
DE Amino acid sequence of cancer associated polypeptide CH8-2a13-1.

PN WO200009655-A2.
PD 24-FEB-2000.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA (USGO) US GOVERNMENT.
Query Match 5.9%; Score 70.5; DB 3; Length 1109;
Best Local Similarity 26.7%; Pred. No. 4.2e+02;
RESULT 658
ID AAM01570 standard; protein, 1159 AA.
DE Protein encoded by CH8-2a13-1, over abundant in cancer cells.
PN WO9639516-A2.
PD 12-DEC-1996.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL RES INST.
Query Match 5.9%; Score 70.5; DB 2; Length 1159;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 659
ID AAM40371 standard; protein, 1159 AA.
DE Human breast cancer protein CH8-2a13-1 from 4.0 kb DNA fragment.
PN WO9738085-A2.
PD 16-OCT-1997.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 5.9%; Score 70.5; DB 2; Length 1159;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 660
ID AAM01571 standard; protein, 1164 AA.
DE Protein encoded by full length CH8-2a13-1, found in cancer cells.
PN WO9639516-A2.
PD 12-DEC-1996.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL RES INST.
Query Match 5.9%; Score 70.5; DB 2; Length 1164;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 661
ID AAM58759 standard; protein, 1164 AA.
DE Human breast cancer gene CH8-2a13-1 protein fragment #3.
PN WO9738085-A2.
PD 16-OCT-1997.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 5.9%; Score 70.5; DB 2; Length 1164;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 662
ID AAY84035 standard; protein, 1367 AA.
DE Amino acid sequence of longest open reading frame of CH8-2a13-1 cDNA.
PN WO200009655-A2.
PD 24-FEB-2000.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
Query Match 5.9%; Score 70.5; DB 3; Length 1367;
Best Local Similarity 26.7%; Pred. No. 5.6e+02;
RESULT 663
ID ADC31466 standard; protein, 268 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1548.
PN WO2003029721-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 70; DB 7; Length 268;
Best Local Similarity 25.4%; Pred. No. 69;
RESULT 664
ID AAU32368 standard; protein, 273 AA.
DE Novel human secreted protein #2859.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 70; DB 4; Length 273;
Best Local Similarity 18.6%; Pred. No. 71;
RESULT 665
ID AAM13671 standard; protein, 309 AA.
DE Peptide #105 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 666
ID ABB32602 standard; peptide, 309 AA.

DE Peptide #108 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 667
ID AAM26070 standard; protein, 309 AA.
DE Peptide #107 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 668
ID ABB27453 standard; peptide, 309 AA.
DE Human peptide #104 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 669
ID ABB18099 standard; protein, 309 AA.
DE Protein #98 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 670
ID AAM65809 standard; protein, 309 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26115.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 671
ID AAM53431 standard; protein, 309 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25536.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 672
ID ABB47455 standard; peptide, 309 AA.
DE Human liver peptide, SEQ ID NO 26103.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 673
ID AAM01421 standard; protein, 309 AA.
DE Peptide #103 encoded by probe for measuring human breast gene expression.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 4; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 674
ID ABB33443 standard; peptide, 309 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25108.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 5.8%; Score 70; DB 5; Length 309;
Best Local Similarity 20.6%; Pred. No. 84;
RESULT 675
ID AAU35202 standard; protein, 316 AA.
DE Enterococcus faecalis cellular proliferation protein #489.

PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 70; DB 4; Length 316;
 Best Local Similarity 20.1%; Pred. No. 86;
 RESULT 676
 ID AAG89296 standard; protein; 354 AA.
 DE Human secreted protein, SEQ ID NO: 416.
 PN WO200142451-A2.
 PD 14-JUN-2001.
 PA (GEST-) GENSET.
 Query Match 5.8%; Score 70; DB 4; Length 354;
 Best Local Similarity 25.4%; Pred. No. 1e+02;
 RESULT 677
 ID ABB08166 standard; protein; 354 AA.
 DE Human cytoskeleton-associated protein (CSAP)-10 (ID: 1568689CD1).
 PN WO200242330-A2.
 PD 30-MAY-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.8%; Score 70; DB 5; Length 354;
 Best Local Similarity 25.4%; Pred. No. 1e+02;
 RESULT 678
 ID ADN08302 standard; protein; 354 AA.
 DE 3T3 cell transformation promoting human protein, SEQ ID 2.
 PN WO2004033493-A1.
 PD 22-APR-2004.
 PA (NEMO-) NEMOGEN LTD.
 Query Match 5.8%; Score 70; DB 8; Length 354;
 Best Local Similarity 25.4%; Pred. No. 1e+02;
 RESULT 679
 ID ABU21164 standard; protein; 359 AA.
 DE Protein encoded by Prokaryotic essential gene #6691.
 PN WO200271183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 70; DB 6; Length 359;
 Best Local Similarity 22.4%; Pred. No. 1e+02;
 RESULT 680
 ID AD116907 standard; protein; 402 AA.
 DE NOVX protein homologue SeqID 443.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 70; DB 5; Length 402;
 Best Local Similarity 20.6%; Pred. No. 1.2e+02;
 RESULT 681
 ID AAM93717 standard; protein; 408 AA.
 DE Human polypeptide, SEQ ID NO: 3663.
 PN EP130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.8%; Score 70; DB 4; Length 408;
 Best Local Similarity 21.0%; Pred. No. 1.2e+02;
 RESULT 682
 ID ADJ1630 standard; protein; 408 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 3663.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REXS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.8%; Score 70; DB 8; Length 408;
 Best Local Similarity 21.0%; Pred. No. 1.2e+02;
 RESULT 683
 ID ABB06069 standard; protein; 428 AA.
 DE Human NS protein sequence SEQ ID NO:161.
 PN WO200206315-A2.
 PD 24-JAN-2002.
 PA (COMP-) COMPUGEN LTD.
 Query Match 5.8%; Score 70; DB 5; Length 428;
 Best Local Similarity 25.4%; Pred. No. 1.3e+02;
 RESULT 684
 ID AAB15721 standard; protein; 438 AA.
 DE Delta130 TRAF-3 deletion isoform.
 PN WO200053629-A1.

PD 14-SEP-2000.
 PA (UYCO-) UNIV COLUMBIA NEW YORK.
 Query Match 5.8%; Score 70; DB 3; Length 438;
 Best Local Similarity 26.4%; Pred. No. 1.4e+02;
 RESULT 685
 ID ABR40829 standard; protein; 485 AA.
 DE Zea mays oil trait related protein sequence SEQ ID NO:421.
 PN WO2003002751-A2.
 PD 09-JAN-2003.
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.
 Query Match 5.8%; Score 70; DB 6; Length 485;
 Best Local Similarity 21.8%; Pred. No. 1.6e+02;
 RESULT 686
 ID ABR40934 standard; protein; 485 AA.
 DE Zea mays oil trait related protein sequence SEQ ID NO:426.
 PN WO2003002751-A2.
 PD 09-JAN-2003.
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.
 Query Match 5.8%; Score 70; DB 6; Length 485;
 Best Local Similarity 21.8%; Pred. No. 1.6e+02;
 RESULT 687
 ID AD116584 standard; protein; 503 AA.
 DE Human NOVX protein to treat human pathological conditions SeqID120.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 70; DB 5; Length 503;
 Best Local Similarity 20.6%; Pred. No. 1.6e+02;
 RESULT 688
 ID ADN42238 standard; protein; 503 AA.
 DE Human novel protein NOV 28.
 PN US2004033493-A1.
 PD 19-FEB-2004.
 PA (TCHE-) TCHEBNEV V T.
 PA (SPYT-) SPYTEK K A.
 PA (ZERH-) ZERHUSEN B D.
 PA (PATY-) PATYURAJAN M.
 PA (SHIM-) SHIMKETS R A.
 PA (LIL/) LI L.
 PA (GANG-) GANGOLI E A.
 PA (PADI-) PADIGARU M.
 PA (ANDE-) ANDERSON D W.
 PA (RAST-) RASTELI L.
 PA (MIL/) MILLER C E.
 PA (GERL-) GERLACH V.
 PA (TAUP-) TAUPIER R J.
 PA (GUSE-) GUSEV V Y.
 PA (COLM-) COLMAN S D.
 PA (WOLE-) WOLENC A R.
 PA (PENA-) PENNA C E A.
 PA (FURT-) FURTAK K.
 PA (GROS-) GROSSE W M.
 PA (ALSO-) ALSOROOK J P.
 PA (LEPL-) LEPLER D M.
 PA (RIEG-) RIEGER D K.
 PA (BURG-) BURGESS C E.
 Query Match 5.8%; Score 70; DB 8; Length 503;
 Best Local Similarity 20.6%; Pred. No. 1.6e+02;
 RESULT 689
 ID ADM07155 standard; protein; 542 AA.
 DE Aspergillus fumigatus Essential For Growth protein #40.
 PN WO2003076464-A2.
 PD 18-SEP-2003.
 PA (FARB-) BAYER CROSCIENCE SA.
 PA (INSP-) INST PASTEUR.
 Query Match 5.8%; Score 70; DB 7; Length 542;
 Best Local Similarity 22.0%; Pred. No. 1.8e+02;
 RESULT 690
 ID ADM07042 standard; protein; 542 AA.
 DE Aspergillus fumigatus Essential For Growth protein #19.
 PN WO2003076464-A2.

PD 18-SEP-2003.
PA (FARB) BAYER CROSCIENCE SA.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 70; DB 7; Length 542;
Best Local Similarity 22.0%; Pred. No. 1.8e+02;
RESULT 691
ID ADP49787 standard; protein; 746 AA.
DE Human 193P1B1V.1.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALDITA-ETD P M.
PA (FARI/) FARIS M.
PA (HUBB/) HUBERT R S.
PA (GBWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match 5.8%; Score 70; DB 8; Length 746;
Best Local Similarity 22.4%; Pred. No. 2.8e+02;
RESULT 692
ID ADP12177 standard; protein; 763 AA.
DE Alloiococcus oltis antigenic protein SEQ ID NO:6536.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 70; DB 6; Length 763;
Best Local Similarity 22.5%; Pred. No. 2.9e+02;
RESULT 693
ID ADP12175 standard; protein; 765 AA.
DE Alloiococcus oltis antigenic protein SEQ ID NO:6538.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 70; DB 6; Length 765;
Best Local Similarity 22.5%; Pred. No. 2.9e+02;
RESULT 694
ID ABU38646 standard; protein; 784 AA.
DE Protein encoded by Prokaryotic essential gene #24173.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 70; DB 6; Length 784;
Best Local Similarity 23.6%; Pred. No. 3e+02;
RESULT 695
ID ADN21025 standard; protein; 806 AA.
DE Bacterial polypeptide #3678.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 70; DB 8; Length 806;
Best Local Similarity 26.5%; Pred. No. 3.1e+02;
RESULT 696
ID ADA89281 standard; protein; 830 AA.
DE Human 1BDBP1 protein SEQ ID NO:4.
PN WO2003052412-A2.
PD 26-JUN-2003.
PA (OXAG-) OXAGEN LTD.
Query Match 5.8%; Score 70; DB 6; Length 830;
Best Local Similarity 21.0%; Pred. No. 3.2e+02;
RESULT 697
ID ADA89279 standard; protein; 836 AA.
DE Human 1BDBP1 protein SEQ ID NO:2.
PN WO2003052412-A2.
PD 26-JUN-2003.
PA (OXAG-) OXAGEN LTD.
Query Match 5.8%; Score 70; DB 6; Length 836;
Best Local Similarity 21.0%; Pred. No. 3.3e+02;
RESULT 698
ID ABU3135 standard; protein; 1417 AA.
DE Protein encoded by Prokaryotic essential gene #8662.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 70; DB 6; Length 1417;
Best Local Similarity 19.3%; Pred. No. 6.8e+02;
RESULT 699
ID ABP73768 standard; protein; 1839 AA.
DE Candida albicans essential protein SEQ ID NO 7605.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 70; DB 5; Length 1839;
Best Local Similarity 26.6%; Pred. No. 9.7e+02;
RESULT 700
ID ADL15088 standard; protein; 2137 AA.
DE Human male bain KIAA0303 protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 5.8%; Score 70; DB 7; Length 2137;
Best Local Similarity 23.9%; Pred. No. 1.2e+03;
RESULT 701
ID AAM78959 standard; protein; 2161 AA.
DE Human protein SEQ ID NO 1621.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 70; DB 4; Length 2161;
Best Local Similarity 23.9%; Pred. No. 1.2e+03;
RESULT 702
ID AAM79943 standard; protein; 2189 AA.
DE Human protein SEQ ID NO 3589.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 70; DB 4; Length 2189;
Best Local Similarity 23.9%; Pred. No. 1.2e+03;
RESULT 703
ID ADM87266 standard; protein; 2432 AA.
DE Human protein SEQ ID NO:359.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.8%; Score 70; DB 8; Length 2432;
Best Local Similarity 23.9%; Pred. No. 1.4e+03;
RESULT 704
ID AAU03503 standard; protein; 2523 AA.
DE Human protein kinase #3.
PN WO200138503-A2.
PD 31-MAY-2001.
PA (SUGB-) SUGEN INC.
Query Match 5.8%; Score 70; DB 5; Length 2523;
Best Local Similarity 23.9%; Pred. No. 1.5e+03;
RESULT 705
ID ABB98406 standard; protein; 2545 AA.
DE Human NOV5, MAST205-like protein.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 70; DB 5; Length 2545;
Best Local Similarity 23.9%; Pred. No. 1.5e+03;
RESULT 706
ID AAJ31558 standard; protein; 6797 AA.
DE Pimaricin biosynthesis associated polypeptide synthase polypeptide.
PN WO200077222-A1.
PD 21-DEC-2000.
PA (STRM-) DSM NV.
Query Match 5.8%; Score 70; DB 4; Length 6797;
Best Local Similarity 25.8%; Pred. No. 5.8e+03;
RESULT 707
ID ABB52647 standard; protein; 277 AA.
DE Escherichia coli polypeptide SEQ ID NO 682.
PN WO200166572-A2.

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PD 13-SEP-2001.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 5.8%; Score 69.5; DB 4; Length 277;
Best Local Similarity 29.7%; Pred. No. 82;
RESULT 708
ID AAM39320 standard; protein; 396 AA.
DE Human polypeptide SEQ ID NO 2465.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 396;
Best Local Similarity 23.2%; Pred. No. 1.3e+02;
RESULT 709
ID ABP73343 standard; protein; 423 AA.
DE Candida albicans essential protein SEQ ID NO 7180.
PN WO200235728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 5; Length 423;
Best Local Similarity 20.8%; Pred. No. 1.5e+02;
RESULT 710
ID AAR33772 standard; protein; 438 AA.
DE Potato tuber PPO PSRP33.
PN WO9302195-A1.
PD 04-FEB-1993.
PA (CSTR ) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.8%; Score 69.5; DB 2; Length 438;
Best Local Similarity 19.3%; Pred. No. 1.5e+02;
RESULT 711
ID ADR58593 standard; protein; 508 AA.
DE Human INTSIG (INTSIG-2), an immunoglobulin like protein.
PN WO2004067712-A2.
PD 12-AUG-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 508;
Best Local Similarity 22.2%; Pred. No. 1.9e+02;
RESULT 712
ID ADD37712 standard; protein; 537 AA.
DE Human adipocyte Selected Interacting Domain (SID) prey protein #1169.
PN WO200290544-A2.
PD 14-NOV-2002.
PA (HYBR-) HYBRIGENICS.
PA (LYNX-) LYNX THERAPEUTICS INC.
Query Match 5.8%; Score 69.5; DB 7; Length 537;
Best Local Similarity 20.6%; Pred. No. 2e+02;
RESULT 713
ID ABU29418 standard; protein; 588 AA.
DE Protein encoded by Prokaryotic essential gene #14945.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 588;
Best Local Similarity 23.5%; Pred. No. 2.3e+02;
RESULT 714
ID ABO76944 standard; protein; 681 AA.
DE Pseudomonas aeruginosa polypeptide #9119.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 681;
Best Local Similarity 23.5%; Pred. No. 2.8e+02;
RESULT 715
ID ADP87685 standard; protein; 747 AA.
DE Rat AMP-activated protein kinase beta 2 subunit protein.
PN WO2004056961-A2.
PD 08-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 747;
Best Local Similarity 27.8%; Pred. No. 3.2e+02;
RESULT 716
ID ADG45228 standard; protein; 775 AA.
DE Mutant Pfu DNA polymerase - T452p.
PN WO2003060144-A2.

PD 24-JUL-2003.
PA (STRA-) STRATAGENE.
Query Match 5.8%; Score 69.5; DB 7; Length 775;
Best Local Similarity 20.1%; Pred. No. 3.4e+02;
RESULT 717
ID ADS21339 standard; protein; 817 AA.
DE Bacterial polypeptide #10372.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 817;
Best Local Similarity 18.3%; Pred. No. 3.6e+02;
RESULT 718
ID AAU90961 standard; protein; 910 AA.
DE DMS:acceptor oxidoreductase alpha subunit.
PN WO200216570-A1.
PD 28-FEB-2002.
PA (UYQU ) UNIV QUEENSLAND.
Query Match 5.8%; Score 69.5; DB 5; Length 910;
Best Local Similarity 22.0%; Pred. No. 4.2e+02;
RESULT 719
ID AAG49832 standard; protein; 1066 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63081.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 1066;
Best Local Similarity 20.5%; Pred. No. 5.2e+02;
RESULT 720
ID AAG49831 standard; protein; 1073 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63080.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 1073;
Best Local Similarity 20.5%; Pred. No. 5.3e+02;
RESULT 721
ID AAG49830 standard; protein; 1086 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63079.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 1086;
Best Local Similarity 20.5%; Pred. No. 5.4e+02;
RESULT 722
ID ABB12337 standard; protein; 1089 AA.
DE Human bone marrow expressed protein SEQ ID NO: 91.
PN WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 1089;
Best Local Similarity 23.3%; Pred. No. 5.4e+02;
RESULT 723
ID ABR71928 standard; protein; 2037 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42576.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 2037;
Best Local Similarity 21.4%; Pred. No. 1.3e+03;
RESULT 724
ID ADU69345 standard; protein; 2041 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1151.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.8%; Score 69.5; DB 7; Length 2041;
Best Local Similarity 19.6%; Pred. No. 1.3e+03;
RESULT 725
ID AAM40027 standard; protein; 2048 AA.
DE Human polypeptide SEQ ID NO 3172.
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PN W020015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.8%; Score 69.5; DB 4; Length 2048;
Pred. No. 1.3e+03;
RESULT 726
ID AD68994 standard; protein; 2270 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID800.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 5.8%; Score 69.5; DB 7; Length 2270;
Pred. No. 1.5e+03;
RESULT 727
ID ABB97596 standard; protein; 2871 AA.
DE Novel human protein SEQ ID NO: 864.
PN W0200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 5.8%; Score 69.5; DB 5; Length 2871;
Pred. No. 2e+03;
RESULT 728
ID ADR90282 standard; peptide; 21 AA.
DE Rice intracellular transport/TPL1-related Ap002882 peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIYUNSU SH.
Query Match
Best Local Similarity 5.7%; Score 69; DB 8; Length 21;
Pred. No. 2.7;
RESULT 729
ID AAW12696 standard; protein; 212 AA.
DE Fibroblast growth factor 13.
PN W09639508-A1.
PD 12-DEC-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 2; Length 212;
Pred. No. 65;
RESULT 730
ID AAW40077 standard; protein; 212 AA.
DE Human FGF-13 protein.
PN US5728546-A.
PD 17-MAR-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 2; Length 212;
Pred. No. 65;
RESULT 731
ID ABB99132 standard; protein; 212 AA.
DE Human fibroblast growth factor FGF13.
PN US2002076748-A1.
PD 20-JUN-2002.
PA (GRENE/) GRENE J M.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 5.7%; Score 69; DB 5; Length 212;
Pred. No. 65;
RESULT 732
ID AAR43338 standard; protein; 214 AA.
DE Completely humanised C4G1 Ig light chain.
PN W09313133-A1.
PD 08-JUL-1993.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 2; Length 214;
Pred. No. 66;
RESULT 733
ID AAW49815 standard; protein; 214 AA.
DE Amino acid sequence of the humanised antibody C4G1 light chain.
PN US5777085-A.
PD 07-JUL-1998.
PA (PROT-) PROTEIN DESIGN LABS INC.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match
Best Local Similarity 5.7%; Score 69; DB 2; Length 214;
Pred. No. 66;
RESULT 734
ID ABR5870 standard; protein; 214 AA.
DE Human immunoglobulin G (IgG) light chain.
PN W02003031464-A2.
PD 17-APR-2003.
PA (NEOS-) NEOS TECHNOLOGIES INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 6; Length 214;
Pred. No. 66;
RESULT 735
ID ADN49727 standard; protein; 214 AA.
DE Human immunoglobulin protein light chain SegID 55.
PN W02004033651-A2.
PD 22-APR-2004.
PA (NEOS-) NEOS TECHNOLOGIES INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 8; Length 214;
Pred. No. 66;
RESULT 736
ID AAG48506 standard; protein; 226 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61260.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.7%; Score 69; DB 3; Length 226;
Pred. No. 71;
RESULT 737
ID AAB49242 standard; protein; 233 AA.
DE Chimeric 4H6 anti-DR4 antibody light chain protein.
PN W0200073349-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.7%; Score 69; DB 4; Length 233;
Pred. No. 74;
RESULT 738
ID ABR55483 standard; protein; 234 AA.
DE CURA05 protein sequence SEQ ID NO:587.
PN W0200283872-A2.
PD 24-OCT-2002.
PA (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
Query Match
Best Local Similarity 5.7%; Score 69; DB 6; Length 234;
Pred. No. 74;
RESULT 739
ID AAR98943 standard; protein; 245 AA.
DE Humanised anti-CD38 monoclonal antibody light chain.
PN W09616990-A1.
PD 06-JUN-1996.
PA (WELL) WELLCOME FOUND LTD.
Query Match
Best Local Similarity 5.7%; Score 69; DB 2; Length 245;
Pred. No. 79;
RESULT 740
ID AAG48505 standard; protein; 265 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61259.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 5.7%; Score 69; DB 3; Length 265;
Pred. No. 88;
RESULT 741
ID ADC23981 standard; protein; 329 AA.
DE Protein sequence (SegID 248) exhibiting nitrate activity.
PN W02003000840-A2.
PD 03-JAN-2003.
PA (DIVE-) DIVERSA CORP.
PA (MADD/) MADSEN D.
Query Match
Best Local Similarity 5.7%; Score 69; DB 7; Length 329;
Pred. No. 1.2e+02;
RESULT 742
ID ADH36082 standard; protein; 329 AA.
DE Chemical process monitoring-related nitrate protein sequence SegID248.
PN W02003098187-A2.
PD 27-NOV-2003.

PA (DIYE-) DIVERSA CORP.
Query Match 5.7%; Score 69; DB 8; Length 329;
Best Local Similarity 24.8%; Pred. No. 1.2e+02;
RESULT 743
ID ADG33763 standard; protein; 329 AA.
DE Nitricase enzyme amino acid sequence SegID248.
PN WO2003097810-A2.
PD 27-NOV-2003.
PA (DIYE-) DIVERSA CORP.
Query Match 5.7%; Score 69; DB 8; Length 329;
Best Local Similarity 24.8%; Pred. No. 1.2e+02;
RESULT 744
ID ADI62380 standard; protein; 329 AA.
DE Nitricase polypeptide #124.
PN WO2003106415-A2.
PD 24-DEC-2003.
PA (DIYE-) DIVERSA CORP.
Query Match 5.7%; Score 69; DB 8; Length 329;
Best Local Similarity 24.8%; Pred. No. 1.2e+02;
RESULT 745
ID ADI64501 standard; protein; 329 AA.
DE Nitricase seq id 125.
PN US2004014195-A1.
PD 22-JAN-2004.
PA (DIYE-) DIVERSA CORP.
Query Match 5.7%; Score 69; DB 8; Length 329;
Best Local Similarity 24.8%; Pred. No. 1.2e+02;
RESULT 746
ID ADF04814 standard; protein; 361 AA.
DE Bacterial polypeptide #927.
PN US605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 69; DB 7; Length 361;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
RESULT 747
ID AB93803 standard; protein; 378 AA.
DE Heridicidally active polypeptide SEQ ID NO 3014.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB-) BAYER AG.
Query Match 5.7%; Score 69; DB 5; Length 378;
Best Local Similarity 23.0%; Pred. No. 1.4e+02;
RESULT 748
ID AAG16813 standard; protein; 395 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17600.
PN EPI033405-A2.
PD 06-SEP-2000.
PA
Query Match 5.7%; Score 69; DB 3; Length 395;
Best Local Similarity 22.7%; Pred. No. 1.5e+02;
RESULT 749
ID AAG16812 standard; protein; 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17599.
PN EPI033405-A2.
PD 06-SEP-2000.
PA
Query Match 5.7%; Score 69; DB 3; Length 415;
Best Local Similarity 22.7%; Pred. No. 1.6e+02;
RESULT 750
ID ADA48422 standard; protein; 417 AA.
DE Rice protein conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 69; DB 6; Length 417;
Best Local Similarity 23.9%; Pred. No. 1.6e+02;
RESULT 751
ID AAG16811 standard; protein; 424 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17598.
PN EPI033405-A2.
PD 06-SEP-2000.
PA
Query Match 5.7%; Score 69; DB 3; Length 424;
Best Local Similarity 22.7%; Pred. No. 1.7e+02;
RESULT 752

ID ABG25955 standard; protein; 425 AA.
DE Novel human diagnostic protein #25946.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 69; DB 4; Length 425;
Best Local Similarity 21.7%; Pred. No. 1.7e+02;
RESULT 753
ID AAB31949 standard; protein; 492 AA.
DE Amino acid sequence of a rice AMP deaminase enzyme.
PN WO200109305-A2.
PD 08-FEB-2001.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.7%; Score 69; DB 4; Length 492;
Best Local Similarity 22.2%; Pred. No. 2.1e+02;
RESULT 754
ID ADA54497 standard; protein; 672 AA.
DE Human protein, SEQ ID 2065.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 69; DB 6; Length 672;
Best Local Similarity 20.5%; Pred. No. 3.2e+02;
RESULT 755
ID AAB92775 standard; protein; 674 AA.
DE Human protein sequence SEQ ID NO:11256.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.7%; Score 69; DB 4; Length 674;
Best Local Similarity 23.6%; Pred. No. 3.2e+02;
RESULT 756
ID AAB31955 standard; protein; 681 AA.
DE Amino acid sequence of a wheat AMP deaminase enzyme.
PN WO200109305-A2.
PD 08-FEB-2001.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.7%; Score 69; DB 4; Length 681;
Best Local Similarity 22.2%; Pred. No. 3.2e+02;
RESULT 757
ID AAB69032 standard; protein; 762 AA.
DE Human polypeptide SEQ ID NO 1079.
PN WO2002070539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 69; DB 5; Length 762;
Best Local Similarity 23.6%; Pred. No. 3.8e+02;
RESULT 758
ID AAB46726 standard; protein; 773 AA.
DE Desulfococcus sp DNA polymerase protein fragment SBQ ID NO 35.
PN WO2000075335-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.7%; Score 69; DB 4; Length 773;
Best Local Similarity 25.0%; Pred. No. 3.8e+02;
RESULT 759
ID AAB87548 standard; protein; 774 AA.
DE A tfu DNA polymerase from Thermococcus funiculans.
PN WO9849274-A1.
PD 05-NOV-1998.
PA (APPL-) APPLIGENE-ONCOR.
Query Match 5.7%; Score 69; DB 2; Length 774;
Best Local Similarity 25.0%; Pred. No. 3.8e+02;
RESULT 760
ID AAB33689 standard; protein; 818 AA.
DE Human structural and cytoskeleton-associated protein (SCAP) #23.
PN WO2002101009-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 69; DB 6; Length 818;

Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 761
ID ADO65069 standard; protein: 842 AA.
DE Novel human protein sequence #42.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 69; DB 8; Length 842;
Best Local Similarity 23.6%; Pred. No. 4.3e+02;
RESULT 762
ID AD146109 standard; protein: 1031 AA.
DE Single stranded nucleic acid cleavage method related protein #4.
PN WO200179481-A2.
PD 25-OCT-2001.
PA (DYAX-) DYAX CORP.
Query Match 5.7%; Score 69; DB 5; Length 1011;
Best Local Similarity 22.1%; Pred. No. 5.7e+02;
RESULT 763
ID ADB64676 standard; protein: 1045 AA.
DE Human protein encoded by clone MESAN2069530.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (RRAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 69; DB 7; Length 1045;
Best Local Similarity 20.6%; Pred. No. 5.8e+02;
RESULT 764
ID AAB68898 standard; protein: 1064 AA.
DE Human HX2004-6 protein.
PN WO200107614-A1.
PD 01-FEB-2001.
PA (CHIR-) CHIRON CORP.
Query Match 5.7%; Score 69; DB 4; Length 1064;
Best Local Similarity 20.6%; Pred. No. 5.9e+02;
RESULT 765
ID ABG65653 standard; protein: 1339 AA.
DE Human breast specific polypeptide, BSP #123.
PN WO200236807-A2.
PD 10-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 5.7%; Score 69; DB 5; Length 1339;
Best Local Similarity 22.1%; Pred. No. 8.1e+02;
RESULT 766
ID AAU30827 standard; protein: 185 AA.
DE Novel human secreted protein #1318.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 185;
Best Local Similarity 23.0%; Pred. No. 61;
RESULT 767
ID ABB12485 standard; protein: 205 AA.
DE Human bone marrow expressed protein SEQ ID NO: 324.
PN WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 205;
Best Local Similarity 25.1%; Pred. No. 71;
RESULT 768
ID ABB70803 standard; protein: 210 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39201.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE-) PE CORP NY.
Query Match 5.7%; Score 68.5; DB 4; Length 210;
Best Local Similarity 27.1%; Pred. No. 73;
RESULT 769
ID AAY87508 standard; protein: 211 AA.
DE Fibroblast growth factor-13 (FGF-13) portion.
PN WO200016704-A1.
PD 30-MAR-2000.
PA (EKOS-) EKOS CORP.
Query Match 5.7%; Score 68.5; DB 3; Length 211;

Best Local Similarity 22.2%; Pred. No. 73;
RESULT 770
ID ABB27575 standard; protein: 283 AA.
DE Protein encoded by prokaryotic essential gene #13102.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 283;
Best Local Similarity 21.2%; Pred. No. 1.1e+02;
RESULT 771
ID AAY94272 standard; protein: 321 AA.
DE Corn arginyl-tRNA synthetase # 1.
PN WO200028057-A2.
PD 18-MAY-2000.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
PA (PRON-) PIONEER HI-BRED INT INC.
Query Match 5.7%; Score 68.5; DB 3; Length 321;
Best Local Similarity 21.2%; Pred. No. 1.3e+02;
RESULT 772
ID AAY58791 standard; protein: 343 AA.
DE Soybean phosphatidic acid phosphatase soyPAP1.
PN WO200005385-A1.
PD 03-FEB-2000.
PA (CALJ-) CALGENE LLC.
Query Match 5.7%; Score 68.5; DB 3; Length 343;
Best Local Similarity 23.3%; Pred. No. 1.4e+02;
RESULT 773
ID ABU08363 standard; protein: 343 AA.
DE Soybean phosphatidic acid phosphatase, soyPAP1.
PN US6495739-B1.
PD 17-DEC-2002.
PA (CALJ-) CALGENE LLC.
Query Match 5.7%; Score 68.5; DB 6; Length 343;
Best Local Similarity 23.3%; Pred. No. 1.4e+02;
RESULT 774
ID ADU49489 standard; protein: 425 AA.
DE Oil-associated gene related protein #989.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR-) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.7%; Score 68.5; DB 8; Length 425;
Best Local Similarity 27.3%; Pred. No. 1.9e+02;
RESULT 775
ID AAW26312 standard; protein: 472 AA.
DE Rat SRCH chaperone protein.
PN US5646249-A.
PD 08-JUL-1997.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 2; Length 472;
Best Local Similarity 22.5%; Pred. No. 2.2e+02;
RESULT 776
ID ABO67710 standard; protein: 551 AA.
DE Klebsiella pneumoniae polypeptide seqid 14227.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 551;
Best Local Similarity 22.6%; Pred. No. 2.7e+02;
RESULT 777
ID AAG77947 standard; protein: 605 AA.
DE Haloperoxidase protein from D. hartlebil.
PN WO200179465-A2.
PD 25-OCT-2001.
PA (NOVO-) NOVOZYMES AS.
PA (MAXY-) MAXIGEN INC.
Query Match 5.7%; Score 68.5; DB 5; Length 605;
Best Local Similarity 24.3%; Pred. No. 3.1e+02;
RESULT 778
ID AAM51613 standard; protein: 605 AA.

DE Dreeschlera hartlebii haloperoxidase.
PN WO200179459-A2.
PD 25-OCT-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.7%; Score 68.5; DB 5; Length 605;
Best Local Similarity 24.3%; Pred. No. 3.1e+02;
RESULT 779
ID ADR6172 standard; protein; 612 AA.
DE Aspergillus fumigatus essential gene protein #222.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.7%; Score 68.5; DB 8; Length 612;
Best Local Similarity 24.8%; Pred. No. 3.2e+02;
RESULT 780
ID ADU50127 standard; protein; 860 AA.
DE Oil-associated gene related protein #1627.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.7%; Score 68.5; DB 8; Length 860;
Best Local Similarity 27.3%; Pred. No. 5e+02;
RESULT 781
ID AAU80135 standard; protein; 1185 AA.
DE Chimeric HIV CTL epitope.
PN WO200224897-A2.
PD 28-MAR-2002.
PA (VIRX-) VIRXSYS.
Query Match 5.7%; Score 68.5; DB 5; Length 1185;
Best Local Similarity 21.9%; Pred. No. 7.8e+02;
RESULT 782
ID AAB33407 standard; protein; 1185 AA.
DE Chimeric HIV CTL epitope.
PN WO200278631-A2.
PD 10-OCT-2002.
PA (VIRX-) VIRXSYS.
Query Match 5.7%; Score 68.5; DB 6; Length 1185;
Best Local Similarity 21.9%; Pred. No. 7.8e+02;
RESULT 783
ID ADN42338 standard; protein; 1879 AA.
DE Human novel proteinNOV 61.
PN US200403493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHENEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATY/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Query Match 5.7%; Score 68.5; DB 8; Length 1879;
Best Local Similarity 19.9%; Pred. No. 1.5e+03;

RESULT 784
ID ADN23045 standard; protein; 4307 AA.
DE Bacterial polypeptide #5698.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 4307;
Best Local Similarity 23.3%; Pred. No. 4.6e+03;
RESULT 785
ID ADN23047 standard; protein; 4307 AA.
DE Bacterial polypeptide #5700.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 4307;
Best Local Similarity 23.3%; Pred. No. 4.6e+03;
RESULT 786
ID ADN23046 standard; protein; 4307 AA.
DE Bacterial polypeptide #5699.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 4307;
Best Local Similarity 23.3%; Pred. No. 4.6e+03;
RESULT 787
ID ADP90274 standard; peptide; 21 AA.
DE Thale cress intracellular transport/TFPI-related FT peptide.
PN JP2004261122-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.6%; Score 68; DB 8; Length 21;
Best Local Similarity 57.1%; Pred. No. 3.5;
RESULT 788
ID ADN47103 standard; protein; 180 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SegID981.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.6%; Score 68; DB 8; Length 180;
Best Local Similarity 25.6%; Pred. No. 67;
RESULT 789
ID AAM00373 standard; protein; 214 AA.
DE Anti-CD18 chimeric antibody MM23 light chain.
PN WO9633208-A1.
PD 24-OCT-1996.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 68; DB 2; Length 214;
Best Local Similarity 23.1%; Pred. No. 85;
RESULT 790
ID AAR22755 standard; protein; 233 AA.
DE Reshaped CD4 antibody light chain CD4VIRET.
PN WO9205274-A.
PD 02-APR-1992.
PA (GORM/) GORMAN S D.
Query Match 5.6%; Score 68; DB 2; Length 233;
Best Local Similarity 21.4%; Pred. No. 96;
RESULT 791
ID ABO82377 standard; protein; 259 AA.
DE Pseudomonas aeruginosa polypeptide #14552.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.6%; Score 68; DB 7; Length 259;
Best Local Similarity 26.1%; Pred. No. 1.1e+02;
RESULT 792
ID ABP73902 standard; protein: 328 AA.
DE Candida albicans essential protein SEQ ID NO 7739.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 68; DB 5; Length 328;
Best Local Similarity 25.0%; Pred. No. 1.5e+02;
RESULT 793
ID AAG18352 standard; protein: 339 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19722.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 339;
Best Local Similarity 23.5%; Pred. No. 1.6e+02;
RESULT 794
ID AAG18351 standard; protein: 378 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19721.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 378;
Best Local Similarity 23.5%; Pred. No. 1.9e+02;
RESULT 795
ID AAG54284 standard; protein: 395 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69196.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 395;
Best Local Similarity 22.7%; Pred. No. 2e+02;
RESULT 796
ID AAG54283 standard; protein: 415 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69195.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 415;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;
RESULT 797
ID AAG54282 standard; protein: 424 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69194.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 424;
Best Local Similarity 22.7%; Pred. No. 2.2e+02;
RESULT 798
ID ADN72579 standard; protein: 424 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 474.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPEDESIGN NV.
Query Match 5.6%; Score 68; DB 8; Length 424;
Best Local Similarity 22.7%; Pred. No. 2.2e+02;
RESULT 799
ID AAB66653 standard; protein: 446 AA.
DE LPL S447X peptide.
PN WO200100220-A2.
PD 04-JAN-2001.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
PA (UYAM-) UNIV AMSTERDAM ACADEMIC HOSPITAL.
Query Match 5.6%; Score 68; DB 4; Length 446;
Best Local Similarity 19.9%; Pred. No. 2.3e+02;
RESULT 800
ID AAB66655 standard; protein: 448 AA.
DE Pre-LPL S447X peptide.
PN WO200100220-A2.
PD 04-JAN-2001.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
PA (UYAM-) UNIV AMSTERDAM ACADEMIC HOSPITAL.
Query Match 5.6%; Score 68; DB 4; Length 448;

Best Local Similarity 19.9%; Pred. No. 2.4e+02;
RESULT 801
ID ADP31773 standard; protein: 449 AA.
DE Plant (A. thaliana) transcription factor polypeptide #3.
PN US2003101481-A1.
PD 29-MAY-2003.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROM M.
PA (HEAR/) HEARD J.
PA (RIEC/) RIECHMANN J. L.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (KEDD/) KEDDIE J.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
Query Match 5.6%; Score 68; DB 7; Length 449;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
RESULT 802
ID ADD5828 standard; protein: 449 AA.
DE Thalecress environmental stress-related protein #93.
PN US2003131386-A1.
PD 10-JUL-2003.
PA (SAMA/) SAMARA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J. L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (BATC/) RATCLIFFE O.
PA (PLIG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
Query Match 5.6%; Score 68; DB 7; Length 449;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
RESULT 803
ID ADD31075 standard; protein: 449 AA.
DE Plant yield-related protein from clone G8.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 5.6%; Score 68; DB 7; Length 449;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
RESULT 804
ID ADI41539 standard; protein: 449 AA.
DE Plant transcription factor #1.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B. K.
PA (RIEC/) RIECHMANN J. L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J. E.
PA (HAAR/) HAARE V.
PA (CREB/) CREELMAN R. A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L. J.
PA (REUB/) REUBER T. L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P. E.
PA (PLIG/) PILGRIM M. L.
PA (DUBE/) DUBEL L. A. N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 5.6%; Score 68; DB 8; Length 449;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
RESULT 805
ID ADO01599 standard; protein: 449 AA.
DE Thalecress transcription factor protein #6.
PN US2004045049-A1.

PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (FINE/) FINEA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIANG/) JIANG C.
PA (SAMA/) SAMARA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBBEL A N.
PA (RATC/) RATCLIFFE O.
PA (KIMI/) KIMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 5.6%; Score 68; DB 8; Length 449;
Best Local Similarity 21.5%; Pred. No. 2.4e+02;
RESULT 806
ID AAG90523 standard; protein; 453 AA.
DE C glutamicum protein fragment SEQ ID NO: 4277.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KICW/) KICOWA HAKKO KOGYO KK.
Query Match 5.6%; Score 68; DB 4; Length 453;
Best Local Similarity 24.7%; Pred. No. 2.4e+02;
RESULT 807
ID AAY81989 standard; protein; 458 AA.
DE Chimeric PCB decomposing enzyme protein #1.
PN JP2000069967-A.
PD 07-MAR-2000.
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 5.6%; Score 68; DB 3; Length 458;
Best Local Similarity 24.3%; Pred. No. 2.4e+02;
RESULT 808
ID AAW93150 standard; protein; 474 AA.
DE Thermotogaerobacter sp. xylanase protein Tecendxyla.
PN US5871730-A.
PD 16-FEB-1999.
PA (UYSH-) UNIV SHERBROOKE.
Query Match 5.6%; Score 68; DB 2; Length 474;
Best Local Similarity 26.2%; Pred. No. 2.5e+02;
RESULT 809
ID AAM68154 standard; protein; 475 AA.
DE Human lipoprotein lipase.
PN WO9831835-A1.
PD 23-JUL-1998.
PA (UYVA-) UNIV MARYLAND BALTIMORE.
PA (UYPI-) UNIV PITTSBURGH.
Query Match 5.6%; Score 68; DB 2; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 810
ID AAY49565 standard; protein; 475 AA.
DE Human prothrombin protein sequence.
PN WO950454-A2.
PD 07-OCT-1999.
PA (WHEH-) WHITEHEAD INST BIOMEDICAL RES.
Query Match 5.6%; Score 68; DB 2; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 811
ID AAB6654 standard; protein; 475 AA.
DE Mature LPL peptide.
PN WO200100220-A2.
PD 04-JAN-2001.
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS BV.
PA (UYAM-) UNIV AMSTERDAM ACADEMIC HOSPITAL.
Query Match 5.6%; Score 68; DB 4; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 812

ID AAO15884 standard; protein; 475 AA.
DE Human lipoprotein lipase (LPL).
PN WO200272604-A2.
PD 19-SEP-2002.
PA (SECU-) SEQUENOM INC.
Query Match 5.6%; Score 68; DB 5; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 813
ID ABB06322 standard; protein; 475 AA.
DE Lipoprotein lipase amino acid sequence.
PN WO200202762-A1.
PD 10-JAN-2002.
PA (MOCH-) MOCHIDA PHARM CO LTD.
Query Match 5.6%; Score 68; DB 5; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 814
ID ADE56914 standard; protein; 475 AA.
DE Human Protein P06858, SEQ ID NO 2769.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 815
ID ADD48644 standard; protein; 475 AA.
DE Human Protein LIHUL, SEQ ID NO 14350.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 816
ID ADD46366 standard; protein; 475 AA.
DE Human Protein LIHUL, SEQ ID NO 12652.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 817
ID ADD46958 standard; protein; 475 AA.
DE Human Protein LIHUL, SEQ ID NO 12644.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 818
ID ADE56906 standard; protein; 475 AA.
DE Human Protein P06858, SEQ ID NO 2761.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 819
ID ADD46962 standard; protein; 475 AA.
DE Human Protein LIHUL, SEQ ID NO 12648.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 820
ID ADE56910 standard; protein; 475 AA.
DE Human Protein P06858, SEQ ID NO 2765.
PN WO2003016475-A2.

PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 68; DB 7; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 821
ID AD089960 standard; protein; 475 AA.
DE Antagonist of cell cycle progression polypeptide #195.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 5.6%; Score 68; DB 8; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 822
ID AD81409 standard; protein; 475 AA.
DE Human NF-kappaB pathway-associated protein SeqID100.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.6%; Score 68; DB 8; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 823
ID ADP23568 standard; protein; 475 AA.
DE PRO polypeptide SEQ ID NO:746.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 68; DB 8; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 824
ID ADQ39643 standard; protein; 475 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1306.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.6%; Score 68; DB 8; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 825
ID ADR73480 standard; protein; 475 AA.
DE Human lipoprotein lipase, LPL, protein.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SURR-) SURROMED INC.
Query Match 5.6%; Score 68; DB 8; Length 475;
Best Local Similarity 19.9%; Pred. No. 2.5e+02;
RESULT 826
ID ADM26514 standard; protein; 506 AA.
DE Hyperthermophile Mechanopyrus kandleri protein #1120.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
Query Match 5.6%; Score 68; DB 7; Length 506;
Best Local Similarity 20.4%; Pred. No. 2.8e+02;
RESULT 827
ID ADM05299 standard; protein; 527 AA.
DE Human protein of the invention SEQ ID NO:3984.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.6%; Score 68; DB 7; Length 527;
Best Local Similarity 20.4%; Pred. No. 2.9e+02;
RESULT 828
ID AAW97757 standard; protein; 585 AA.
DE S-region transfer activity-70 (SRTA-70).
PN WO9903991-A1.
PD 28-JAN-1999.
PA (RBGC) UNIV CALIFORNIA.
Query Match 5.6%; Score 68; DB 2; Length 585;
Best Local Similarity 21.1%; Pred. No. 3.4e+02;
RESULT 829
ID AAU27756 standard; protein; 585 AA.

DE Human full-length polypeptide sequence #81.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 68; DB 4; Length 585;
Best Local Similarity 20.4%; Pred. No. 3.4e+02;
RESULT 830
ID ABW81228 standard; protein; 585 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81956, SEQ:3162.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 68; DB 8; Length 585;
Best Local Similarity 20.4%; Pred. No. 3.4e+02;
RESULT 831
ID ADP99182 standard; protein; 603 AA.
DE SNAP70, SEQ ID 188.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 5.6%; Score 68; DB 8; Length 603;
Best Local Similarity 20.4%; Pred. No. 3.5e+02;
RESULT 832
ID AAY38833 standard; protein; 623 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF23.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.6%; Score 68; DB 2; Length 623;
Best Local Similarity 22.6%; Pred. No. 3.7e+02;
RESULT 833
ID ADN9664 standard; protein; 687 AA.
DE Novel human protein sequence #480.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.6%; Score 68; DB 8; Length 687;
Best Local Similarity 29.0%; Pred. No. 4.2e+02;
RESULT 834
ID AAB67571 standard; protein; 737 AA.
DE Amino acid sequence of a human hydrolytic enzyme HYENZ3.
PN WO200116334-A2.
PD 08-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.6%; Score 68; DB 4; Length 737;
Best Local Similarity 20.5%; Pred. No. 4.7e+02;
RESULT 835
ID AAW95332 standard; protein; 738 AA.
DE Human phospholipase A2 activating protein (PLAP).
PN WO9856400-A1.
PD 17-DEC-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 5.6%; Score 68; DB 2; Length 738;
Best Local Similarity 17.2%; Pred. No. 4.7e+02;
RESULT 836
ID ABB64096 standard; protein; 762 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19080.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 68; DB 4; Length 762;
Best Local Similarity 21.6%; Pred. No. 4.9e+02;
RESULT 837
ID AAR72798 standard; protein; 780 AA.
DE Phospholipase D.
PN WO9509234-A1.
PD 06-APR-1995.
PA (NISB) JAPAN TOBACCO INC.
Query Match 5.6%; Score 68; DB 2; Length 780;
Best Local Similarity 22.9%; Pred. No. 5e+02;
RESULT 838
ID AAG46295 standard; protein; 868 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58227.

PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 868;
Best Local Similarity 20.6%; Pred. No. 5.8e+02;
RESULT 839
ID ADK17029 standard; protein; 870 AA.
DE Nanorhizom euglans cancer-associated (CA) protein #490.
PN MO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.6%; Score 68; DB 8; Length 870;
Best Local Similarity 21.6%; Pred. No. 5.8e+02;
RESULT 840
ID AAG66294 standard; protein; 989 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58226.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 989;
Best Local Similarity 20.6%; Pred. No. 7e+02;
RESULT 841
ID AAG45673 standard; protein; 1032 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57369.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 1032;
Best Local Similarity 20.9%; Pred. No. 7.4e+02;
RESULT 842
ID ABG23220 standard; protein; 1033 AA.
DE Novel human diagnostic protein #23211.
PN MO200175067-AA.
PD 11-OCT-2001.
PA (HSE-) HSESEQ INC.
Query Match 5.6%; Score 68; DB 4; Length 1033;
Best Local Similarity 40.0%; Pred. No. 7.4e+02;
RESULT 843
ID AAG45672 standard; protein; 1045 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57368.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 1045;
Best Local Similarity 20.9%; Pred. No. 7.5e+02;
RESULT 844
ID AAG66293 standard; protein; 1065 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58225.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 1065;
Best Local Similarity 20.6%; Pred. No. 7.7e+02;
RESULT 845
ID AAG45671 standard; protein; 1090 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57367.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 68; DB 3; Length 1090;
Best Local Similarity 20.9%; Pred. No. 8e+02;
RESULT 846
ID AB85329 standard; protein; 1468 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22779.
PN MO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.6%; Score 68; DB 4; Length 1468;
Best Local Similarity 22.1%; Pred. No. 1.2e+03;
RESULT 847
ID AAG67554 standard; protein; 1523 AA.
DE A Tfu DNA polymerase (and inteins).
PN MO9849274-A1.
PD 05-NOV-1998.
PA (APPL-) APPLIGENE-ONCOR.
Query Match 5.6%; Score 68; DB 2; Length 1523;
Best Local Similarity 27.8%; Pred. No. 1.3e+03;
RESULT 848
ID ABB09511 standard; protein; 1661 AA.

DE Human set binding factor SBF-1-like NOV3b protein, SBQ ID NO:20.
PN MO200253742-A2.
PD 11-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 68; DB 5; Length 1681;
Best Local Similarity 29.0%; Pred. No. 1.4e+03;
RESULT 849
ID AD010061 standard; protein; 1681 AA.
DE Novel human protein NOV3b.
PN US2004052806-A1.
PD 18-MAR-2004.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOOROOK J P.
PA (TCHE/) TCHEBNEV V T.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K A.
PA (PAT/) PATURAJAN M.
PA (GROS/) GROSSE W M.
PA (LEPL/) LEPLAY D M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LITL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S R.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALVANKAR U M.
PA (ROTH/) ROTHENBERG M E.
PA (STON/) STONE D J.
PA (BOLD/) BOLDOG F L.
PA (CHOX/) CHO X.
PA (SHEN/) SHENOY S G.
Query Match 5.6%; Score 68; DB 8; Length 1681;
Best Local Similarity 29.0%; Pred. No. 1.4e+03;
RESULT 850
ID ABB09510 standard; protein; 1723 AA.
DE Human set binding factor SBF-1-like NOV3a protein, SBQ ID NO:18.
PN MO200253742-A2.
PD 11-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 68; DB 5; Length 1723;
Best Local Similarity 29.0%; Pred. No. 1.5e+03;
RESULT 851
ID AD010059 standard; protein; 1723 AA.
DE Novel human protein NOV3a.
PN US2004052806-A1.
PD 18-MAR-2004.
PA (KEKU/) KEKUDA R.
PA (ALSO/) ALSOOROOK J P.
PA (TCHE/) TCHEBNEV V T.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K A.
PA (PAT/) PATURAJAN M.
PA (GROS/) GROSSE W M.
PA (LEPL/) LEPLAY D M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LITL/) LI L.
PA (GORM/) GORMAN L.
PA (EDIN/) EDINGER S R.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALVANKAR U M.
PA (ROTH/) ROTHENBERG M E.
PA (STON/) STONE D J.
PA (BOLD/) BOLDOG F L.
PA (CHOX/) CHO X.
PA (SHEN/) SHENOY S G.

PA (ANDE/) ANDERSON D W.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (EISE/) EISEN A.
Query Match 5.6%; Score 68; DB 8; Length 1723;
Best Local Similarity 29.0%; Pred. No. 1.5e+03;
RESULT 852
ID ABG66751 standard; protein; 1867 AA.
DE Human novel polypeptide #85.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSB-) HYSBQ INC.
Query Match 5.6%; Score 68; DB 5; Length 1867;
Best Local Similarity 29.0%; Pred. No. 1.7e+03;
RESULT 853
ID AAG79726 standard; protein; 1867 AA.
DE Human KPP-4, Incyte ID No. 2080788CD1.
PN WO200290530-A2.
PD 14-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.6%; Score 68; DB 6; Length 1867;
Best Local Similarity 29.0%; Pred. No. 1.7e+03;
RESULT 854
ID ADE28321 standard; protein; 1893 AA.
DE Human KPP protein - SEQ ID 32.
PN WO2003080805-A2.
PD 02-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.6%; Score 68; DB 8; Length 1893;
Best Local Similarity 29.0%; Pred. No. 1.7e+03;
RESULT 855
ID ADJ50993 standard; protein; 1929 AA.
DE Human novel protein NOV23a.
PN US2004030096-A1.
PD 12-FEB-2004.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (EDIN/) EDINGER S R.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (ZHON/) ZHONG M.
PA (PAT/) PATTURAJAN M.
PA (MILL/) MILLER C E.
PA (JIWW/) JI W.
PA (PENA/) PENA C E A.
PA (BURG/) BURGESS C E.
PA (SCIO/) SCIORE P.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (CASM/) CASMAN S J.
PA (ROTH/) ROTHENBERG M E.
PA (MALV/) MALYANKAR U M.
PA (BOLD/) BOLDOS F L.
Query Match 5.6%; Score 68; DB 8; Length 1929;
Best Local Similarity 29.0%; Pred. No. 1.7e+03;
RESULT 856
ID AAM67738 standard; protein; 2476 AA.
DE Pig p105 zona pellucida-binding protein.
PN US5851817-A.
PD 22-DEC-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 5.6%; Score 68; DB 2; Length 2476;
Best Local Similarity 25.9%; Pred. No. 2.5e+03;
RESULT 857
ID ABW73703 standard; protein; 120 AA.
DE DNA clone originating in barley containing SNP sequence #113.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UTNT-) UNIV JAPAN OKAYAMA.
Query Match 5.6%; Score 67.5; DB 7; Length 120;
Best Local Similarity 22.4%; Pred. No. 44;

RESULT 858
ID ABW73939 standard; protein; 158 AA.
DE DNA clone originating in barley containing SNP sequence #349.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UTNT-) UNIV JAPAN OKAYAMA.
Query Match 5.6%; Score 67.5; DB 7; Length 158;
Best Local Similarity 22.4%; Pred. No. 64;
RESULT 859
ID ADA11728 standard; protein; 164 AA.
DE Human novel secreted protein associated polypeptide #406.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 67.5; DB 6; Length 164;
Best Local Similarity 20.4%; Pred. No. 68;
RESULT 860
ID AAY36329 standard; protein; 165 AA.
DE Human secreted protein encoded by gene 106.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 67.5; DB 2; Length 165;
Best Local Similarity 20.4%; Pred. No. 68;
RESULT 861
ID ADA11728 standard; protein; 165 AA.
DE Human novel secreted protein, SEQ ID NO 256.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 67.5; DB 6; Length 165;
Best Local Similarity 20.4%; Pred. No. 68;
RESULT 862
ID ABU35496 standard; protein; 277 AA.
DE Protein encoded by Prokaryotic essential gene #21023.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 67.5; DB 6; Length 277;
Best Local Similarity 26.8%; Pred. No. 1.4e+02;
RESULT 863
ID AAY93289 standard; protein; 309 AA.
DE Amino acid sequence of a polypeptide of a Neisseria pathogenic strain.
PN WO200026375-A2.
PD 11-MAY-2000.
PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 5.6%; Score 67.5; DB 3; Length 309;
Best Local Similarity 23.4%; Pred. No. 1.6e+02;
RESULT 864
ID AAB66268 standard; protein; 497 AA.
DE Murine TANGO 272 SEQ ID NO: 17.
PN WO200100673-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.6%; Score 67.5; DB 4; Length 497;
Best Local Similarity 21.7%; Pred. No. 3.1e+02;
RESULT 865
ID AAR80505 standard; protein; 512 AA.
DE S. lividans protease P5-4.
PN WO9517512-A2.
PD 29-JUN-1995.
PA (CANG-) CANGENE CORP.
Query Match 5.6%; Score 67.5; DB 2; Length 512;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 866
ID AAM87797 standard; protein; 512 AA.
DE Protease encoded by clone P5-4.
PN US5856166-A.
PD 05-JAN-1999.
PA (CANG-) CANGENE CORP.
Query Match 5.6%; Score 67.5; DB 2; Length 512;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;

RESULT 867
ID AAY40912 standard; protein; 512 AA.
DE Ara h 3 allergen sequence.
PN WO99455961-A1.
PD 16-SEP-1999.
PA (UNIVAR-) UNIV ARKANSAS.
Query Match 5.6%; Score 67.5; DB 2; Length 512;
Best Local Similarity 20.2%; Pred. No. 3.2e+02;
RESULT 868
ID AAB19229 standard; protein; 512 AA.
DE A subtilisin-like polypeptide (Ssp) designated p5-4.
PN US6127144-A.
PD 03-OCT-2000.
PA (CANG-) CANGENE CORP.
Query Match 5.6%; Score 67.5; DB 3; Length 512;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 869
ID ABG27419 standard; protein; 538 AA.
DE Novel human diagnostic protein #27410.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67.5; DB 4; Length 538;
Best Local Similarity 22.5%; Pred. No. 3.4e+02;
RESULT 870
ID ADC0123 standard; protein; 550 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1277.
PN JF2002355074-A.
PD 10-DEC-2002.
PA (UYTYS-) UNIV TSUKUBA.
Query Match 5.6%; Score 67.5; DB 7; Length 550;
Best Local Similarity 23.6%; Pred. No. 3.6e+02;
RESULT 871
ID AAR39554 standard; protein; 596 AA.
DE deduced amino acid sequence encoded by tomato polyphenol oxidase (PPO)
PN CDNA PPPO-T2.
PD WO9315599-A1.
PD 19-AUG-1993.
PA (CORR) CORNELL RES FOUND INC.
Query Match 5.6%; Score 67.5; DB 2; Length 596;
Best Local Similarity 20.2%; Pred. No. 4e+02;
RESULT 872
ID AAB30862 standard; protein; 596 AA.
DE Amino acid sequence of tomato polyphenol oxidase (PPO) PPPO-T2.
PN US6160204-A.
PD 12-DEC-2000.
PA (CORR) CORNELL RES FOUND INC.
Query Match 5.6%; Score 67.5; DB 4; Length 596;
Best Local Similarity 20.2%; Pred. No. 4e+02;
RESULT 873
ID AAB92953 standard; protein; 609 AA.
DE Human protein sequence SEQ ID NO:11635.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.6%; Score 67.5; DB 4; Length 609;
Best Local Similarity 20.4%; Pred. No. 4.1e+02;
RESULT 874
ID ADA11709 standard; protein; 609 AA.
DE Human novel secreted protein, SEQ ID NO 237.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HDMAN-) HDMAN GENOME SCI INC.
Query Match 5.6%; Score 67.5; DB 6; Length 609;
Best Local Similarity 20.4%; Pred. No. 4.1e+02;
RESULT 875
ID ABU11592 standard; protein; 650 AA.
DE Human MDPF polypeptide SEQ ID 539.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.6%; Score 67.5; DB 6; Length 650;
Best Local Similarity 20.4%; Pred. No. 4.5e+02;

RESULT 876
ID ADK62366 standard; protein; 706 AA.
DE Disease treating protein complex-derived protein #309.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 67.5; DB 7; Length 706;
Best Local Similarity 21.3%; Pred. No. 5e+02;
RESULT 877
ID ADQ38173 standard; protein; 723 AA.
DE Canine I-pBE protein SEQ ID NO:2.
PN WO200405893-A2.
PD 15-JUL-2004.
PA (PHRA) PHARMACIA & UPJOHN CO.
Query Match 5.6%; Score 67.5; DB 8; Length 723;
Best Local Similarity 23.1%; Pred. No. 5.2e+02;
RESULT 878
ID ABJ28129 standard; protein; 774 AA.
DE Protein encoded by Prokaryotic essential gene #13656.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 67.5; DB 6; Length 774;
Best Local Similarity 24.0%; Pred. No. 5.7e+02;
RESULT 879
ID AAE05723 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase variant K758C+I914C.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 880
ID AAE05727 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase variant H286C+T148C.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 881
ID AAE05725 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase variant I897C+S819C.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 882
ID AAE05726 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase variant P525C+E499C.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 883
ID AAE05724 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase variant T916C+A765C.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 884
ID AAE05689 standard; protein; 921 AA.
DE Bacillus acidopululiticus pullulanase promozyme.
PN WO200151620-A2.
PD 19-JUL-2001.
PA (NOVO) NOVOZYMES AS.
Query Match 5.6%; Score 67.5; DB 4; Length 921;
Best Local Similarity 22.5%; Pred. No. 7.2e+02;
RESULT 885

ID AAY24150 standard; protein; 2270 AA.
DE Candida albicans acetyl CoA carboxylase.
PN W09932635-A1.
PD 01-JUL-1999.
PA (ZENEC) ZENEC LTD.
Query Match 5.6%; Score 67.5; DB 2; Length 2270;
Best Local Similarity 20.5%; Pred. No. 2.5e+03;
RESULT 886
ID AAR98836 standard; protein; 157 AA.
DE CD40 associated protein (CAP)-1 TRAF domain (residues 384-540).
PN W09616665-A1.
PD 06-JUN-1996.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 5.6%; Score 67; DB 2; Length 157;
Best Local Similarity 26.2%; Pred. No. 72;
RESULT 887
ID AAR63121 standard; protein; 158 AA.
DE ORF1 gene prod. involved in biotin synthesis (pB030A-15/9).
PN W09408023-A2.
PD 14-APR-1994.
PA (LONZ) LONZA AG.
Query Match 5.6%; Score 67; DB 2; Length 158;
Best Local Similarity 25.0%; Pred. No. 73;
RESULT 888
ID AAR98834 standard; protein; 181 AA.
DE CD40 associated protein (CAP)-1 clone pACT-121 (residues 363-543).
PN W09616665-A1.
PD 06-JUN-1996.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 5.6%; Score 67; DB 2; Length 181;
Best Local Similarity 26.2%; Pred. No. 88;
RESULT 889
ID AAR30776 standard; protein; 214 AA.
DE H5216-158 murine anti-CD18 antibody light chain.
PN W09222653-A1.
PD 23-DEC-1992.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 2; Length 214;
Best Local Similarity 23.3%; Pred. No. 1.1e+02;
RESULT 890
ID AAB07003 standard; protein; 228 AA.
DE Human TRAF3(NC)-CA21 protein.
PN W020002670-A1.
PD 11-MAY-2000.
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
Query Match 5.6%; Score 67; DB 3; Length 228;
Best Local Similarity 26.2%; Pred. No. 1.2e+02;
RESULT 891
ID ADS34617 standard; protein; 250 AA.
DE POSH protein associated protein #124.
PN W02004078130-A2.
PD 16-SEP-2004.
PA (PROT-) PROTEOLOGICS INC.
Query Match 5.6%; Score 67; DB 8; Length 250;
Best Local Similarity 21.8%; Pred. No. 1.4e+02;
RESULT 892
ID AAM40139 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 3284.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 258;
Best Local Similarity 19.0%; Pred. No. 1.4e+02;
RESULT 893
ID AAY79565 standard; protein; 282 AA.
DE Human TRAF3 delta-300 mutant.
PN W0200023590-A2.
PD 27-APR-2000.
PA (GROU) UNIV GEORGETOWN MEDICAL CENT.
Query Match 5.6%; Score 67; DB 3; Length 282;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
RESULT 894
ID ADS34580 standard; protein; 300 AA.

DE POSH protein associated protein #108.
PN W02004078130-A2.
PD 16-SEP-2004.
PA (PROT-) PROTEOLOGICS INC.
Query Match 5.6%; Score 67; DB 8; Length 300;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 895
ID ABU49019 standard; protein; 330 AA.
DE Protein encoded by Prokaryotic essential gene #34546.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 67; DB 6; Length 330;
Best Local Similarity 25.2%; Pred. No. 2e+02;
RESULT 896
ID ABG07578 standard; protein; 337 AA.
DE Novel human diagnostic protein #7569.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 337;
Best Local Similarity 26.1%; Pred. No. 2.1e+02;
RESULT 897
ID ABG0104 standard; protein; 337 AA.
DE Novel human diagnostic protein #95.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 337;
Best Local Similarity 26.1%; Pred. No. 2.1e+02;
RESULT 898
ID AAB15722 standard; protein; 347 AA.
DE Delta221 TRAF-3 deletion isoform.
PN W0200053629-A1.
PD 14-SEP-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 3; Length 347;
Best Local Similarity 26.2%; Pred. No. 2.2e+02;
RESULT 899
ID ABBM0453 standard; protein; 354 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80993, SEQ:1142.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 354;
Best Local Similarity 24.9%; Pred. No. 2.2e+02;
RESULT 900
ID AAW04871 standard; protein; 372 AA.
DE Phosphorylation deficient cyclin-dependent kinase-like protein.
PN W09628555-A1.
PD 19-SEP-1996.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 5.6%; Score 67; DB 2; Length 372;
Best Local Similarity 21.6%; Pred. No. 2.4e+02;
RESULT 901
ID AAW04869 standard; protein; 372 AA.
DE Cyclin-dependent kinase-like protein PITARE.
PN W09628555-A1.
PD 19-SEP-1996.
PA (UYJE-) UNIV JEFFERSON THOMAS.
Query Match 5.6%; Score 67; DB 2; Length 372;
Best Local Similarity 21.6%; Pred. No. 2.4e+02;
RESULT 902
ID AAT75107 standard; protein; 372 AA.
DE Cell cycle dependent kinase 9 (CDK9).
PN W0200198524-A2.
PD 27-DEC-2001.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 5.6%; Score 67; DB 5; Length 372;
Best Local Similarity 21.6%; Pred. No. 2.4e+02;
RESULT 903
ID ABU62606 standard; protein; 372 AA.
DE Human P-TEFb protein, CDK9.

PN US2003039658-A1.
PD 27-FEB-2003.
PA (ESTA/) ESTABLE M.
PA (ROED/) ROEDER R A.
Query Match
Best Local Similarity 5.6%; Score 67; DB 6; Length 372;
Pred. No. 2.4e+02;
ID ADF45045 standard; protein; 372 AA.
DE Human kinase CDK9.
PN WO2003081210-A2.
PD 02-OCT-2003.
PA (SUDE-) SUDESSIS PHARM INC.
Query Match
Best Local Similarity 5.6%; Score 67; DB 7; Length 372;
Pred. No. 2.4e+02;
RESULT 905
ID ADH09516 standard; protein; 372 AA.
DE Human host factor protein; SEQ ID No 44.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 906
ID ADH09519 standard; protein; 372 AA.
DE Human host factor protein; SEQ ID No 47.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 907
ID ADH09518 standard; protein; 372 AA.
DE Human host factor protein; SEQ ID No 46.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 908
ID ADH09517 standard; protein; 372 AA.
DE Human host factor protein; SEQ ID No 45.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 909
ID ADH09521 standard; protein; 372 AA.
DE Human host factor protein; SEQ ID No 49.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 910
ID ADF74343 standard; protein; 372 AA.
DE Human cyclin-dependent kinase 9 (CDK9).
PN US2004110140-A1.
PD 10-JUN-2004.
PA (ISTS-) ISTIS PHARM INC.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 372;
Pred. No. 2.4e+02;
RESULT 911
ID ADF04102 standard; protein; 388 AA.
DE Bacterial polypeptide #15.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 5.6%; Score 67; DB 7; Length 388;
Pred. No. 2.5e+02;
RESULT 912
ID ADI43316 standard; protein; 396 AA.
DE Plant transcription factor #577.

PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAR/) HAARE V.
PA (CREB/) CREBLMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PLUG/) PLUGRIM M L.
PA (DOBE/) DOBEL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 396;
Pred. No. 2.6e+02;
RESULT 913
ID ADY48230 standard; protein; 396 AA.
DE Polypeptide sequence #280 useful in producing transgenic plants.
PN US200333670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match
Best Local Similarity 5.6%; Score 67; DB 8; Length 396;
Pred. No. 2.6e+02;
RESULT 914
ID AAM80942 standard; protein; 412 AA.
DE Human heart lecithin-cholesterol acyltransferase-like protein 3.
PN WO9846767-A1.
PD 22-OCT-1998.
PA (TAKE/) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 5.6%; Score 67; DB 2; Length 412;
Pred. No. 2.7e+02;
RESULT 915
ID AAY41708 standard; protein; 412 AA.
DE Human PRO540 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 67; DB 2; Length 412;
Pred. No. 2.7e+02;
RESULT 916
ID AAB19579 standard; protein; 412 AA.
DE Human PRO540 used to treat ocular disease.
PN WO200053760-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 67; DB 3; Length 412;
Pred. No. 2.7e+02;
RESULT 917
ID AAB44264 standard; protein; 412 AA.
DE Human PRO540 (UNQ341) protein sequence SEQ ID NO:157.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 67; DB 3; Length 412;
Pred. No. 2.7e+02;
RESULT 918
ID AAM93359 standard; protein; 412 AA.
DE Human polypeptide, SEQ ID NO: 2917.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 5.6%; Score 67; DB 4; Length 412;
Pred. No. 2.7e+02;
RESULT 919
ID AAB50954 standard; protein; 412 AA.
DE Human PRO540 protein.
PN WO200073348-A2.

PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 4; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 920
ID AAB93243 standard; protein; 412 AA.
DE Human protein sequence SEQ ID NO:12251.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.6%; Score 67; DB 4; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 921
ID ABG34036 standard; protein; 412 AA.
DE Human PRO peptide #7.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 5; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 922
ID ABO25210 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 923
ID ABU72216 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 924
ID ABU71420 standard; protein; 412 AA.
DE Human neoplasia inhibiting PRO polypeptide PRO540.
PN US2002192209-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 925
ID ABH84896 standard; protein; 412 AA.
DE Human secreted and transmembrane polypeptide PRO540.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 926
ID ABU61094 standard; protein; 412 AA.
DE Human PRO540 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 927
ID ABH80363 standard; protein; 412 AA.
DE Human secreted/transmembrane protein PRO540.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 928
ID ADA01282 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 929
ID ADA43711 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 930
ID ADA43479 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 931
ID ADA24696 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 932
ID ADA01154 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 933
ID ABO19665 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 934
ID ADA12357 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 935
ID ABO19556 standard; protein; 412 AA.
DE Novel human secreted and transmembrane polypeptide #24.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 6; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 936
ID ADA01038 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 937
ID ADA43595 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;

Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 938
ID ADA06857 standard; protein; 412 AA.
DE Human PRO polypeptide #1.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 939
ID ADA08345 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 940
ID ADB99638 standard; protein; 412 AA.
DE Human PRO polypeptide SEQ ID 14.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 941
ID ADB86921 standard; protein; 412 AA.
DE Human PRO polypeptide #1.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 942
ID ADB66076 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 943
ID ADB73663 standard; protein; 412 AA.
DE Human PRO polypeptide #24.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 944
ID ADB99754 standard; protein; 412 AA.
DE Human PRO polypeptide SEQ ID 14.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 945
ID ADB76379 standard; protein; 412 AA.
DE Human PRO polypeptide #24.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 946
ID ADB99409 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;

RESULT 947
ID ADB65960 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 948
ID ADC43805 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 949
ID ADC61565 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 950
ID ADC63529 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 951
ID ADC66629 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 952
ID ADC68753 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 953
ID ADC62813 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 954
ID ADC67878 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 955
ID ADC41198 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;

ID ADC67253 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 957
ID ADC23358 standard; protein; 412 AA.
DE Human transmembrane PRO polypeptide (Segid 14).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 958
ID ADC26051 standard; protein; 412 AA.
DE Human PRO540 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 959
ID ADC62189 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US20030731624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 960
ID ADC41822 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 961
ID ADE04878 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 962
ID ADE11184 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 963
ID ADB49191 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 964
ID ADB8115 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 965
ID ADE35245 standard; protein; 412 AA.

DE Human secreted/transmembrane protein, PRO540.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 966
ID ADE16359 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 967
ID ADD2974 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 968
ID ADD95410 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 969
ID ADE06340 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 970
ID ADE38115 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 971
ID ADD72332 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 972
ID ADD8231 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 973
ID ADE16983 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 974
ID ADD90812 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.

PN US2003073186-A1.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 975
ID ADP46997 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 976
ID ADP9367 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 977
ID ADG06460 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 978
ID ADG14400 standard; protein; 412 AA.
DE Human ILPL, SEQ ID 14.
PN WO2003078624-A1.
PD 25-SEP-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 979
ID ADG05411 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 980
ID ADG52754 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 981
ID ADG60074 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 982
ID ADG82412 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 983
ID ADI60834 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003077700-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 7; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 984
ID ADG51665 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 985
ID ADG51781 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 986
ID ADG37639 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 987
ID ADG37523 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 988
ID ADG95294 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 989
ID ADG37994 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 990
ID ADG76083 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 991
ID ADG39406 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 992
ID ADG04210 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003096364-A1.
PD 22-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 993
ID AD839807 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 994
ID AD819672 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 995
ID AD877250 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US200312466-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 996
ID AD865358 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 997
ID AD848491 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 998
ID AD875967 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 999
ID AD837878 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1000
ID AD864488 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1001
ID AD838823 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.

Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1002
ID AD851897 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1003
ID AD890928 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1004
ID AD838707 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1005
ID AD837407 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1006
ID AD806224 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1007
ID AD890083 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1008
ID AD838591 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1009
ID AD839522 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1010
ID AD89127 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
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Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1011
ID ADE88894 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138699-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1012
ID ADE19788 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1013
ID ADE77366 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN 03-JUL-2003.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1014
ID ADE65242 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1015
ID ADE39290 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN 26-JUN-2003.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1016
ID ADE38475 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN 05-JUN-2003.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FITV/) FITVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERLITSSEN M E.
PA (GODD/) GODDARD A.
PA (GIRM/) GIRMALDI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1017
ID ADE89592 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FITV/) FITVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERLITSSEN M E.
PA (GODD/) GODDARD A.
PA (GIRM/) GIRMALDI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1018
ID ADE61232 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1019
ID ADF39924 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1020
ID ADF45720 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1021
ID ADF24116 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1022
ID ADF40548 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1023
ID ADF23492 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1024
ID ADF33475 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1025
ID ADF26942 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
```

Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1026
ID ADF27578 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1027
ID ADF41172 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1028
ID ADF32851 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1029
ID ADF25217 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1030
ID ADF26318 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1031
ID ADF34107 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1032
ID ADF46344 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1033
ID ADF11028 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1034
ID ADG10912 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;

RESULT 1035
ID ADH31440 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1036
ID ADH3868 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1037
ID ADH29323 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1038
ID ADH23626 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1039
ID ADH26956 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1040
ID ADG50330 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1041
ID ADH38224 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1042
ID ADH26840 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1043
ID ADG49706 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1044

ID ADG51578 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US200315908-A1.
PD 20-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1045
ID ADH38108 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1046
ID ADG49082 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1047
ID ADH38804 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1048
ID ADG48458 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1049
ID ADH23742 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1050
ID ADH40118 standard; protein; 412 AA.
DE Human PRO540 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1051
ID ADH40002 standard; protein; 412 AA.
DE Human PRO540 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1052
ID ADH31324 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1053
ID ADH29202 standard; protein; 412 AA.

DE Human secreted/transmembrane polypeptide PRO540.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1054
ID ADH49417 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1055
ID ADG50954 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1056
ID ADH51881 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1057
ID ADH49736 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1058
ID ADH52337 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1059
ID ADG58898 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1060
ID ADH52453 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1061
ID ADH58450 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1062
ID ADH51765 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.

PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1063
ID ADG62354 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1064
ID ADH58326 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1065
ID ADI13523 standard; protein; 412 AA.
DE Novel human secreted and transmembrane protein PRO540.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1066
ID ADH25379 standard; protein; 412 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:157.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1067
ID ADK00779 standard; protein; 412 AA.
DE Human PRO polypeptide #7.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1068
ID ADI08520 standard; protein; 412 AA.
DE Human secreted/transmembrane polypeptide PRO540.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1069
ID ADJ30884 standard; protein; 412 AA.
DE Human protein encoded by a full length cDNA clone SegID 2917.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1070
ID ADM17156 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1071
ID ADL06990 standard; protein; 412 AA.
DE Human secreted/transmembrane protein, PRO540.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1072
ID ADRI4577 standard; protein; 412 AA.
DE Human NF-kappaB pathway-associated protein SegID578.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.6%; Score 67; DB 8; Length 412;
Best Local Similarity 21.2%; Pred. No. 2.7e+02;
RESULT 1073
ID AAG17339 standard; protein; 463 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18320.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (CROP-) CROPDISEIGN NV.
Query Match 5.6%; Score 67; DB 8; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1074
ID AAG42685 standard; protein; 463 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53261.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 5; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1075
ID AAG17338 standard; protein; 465 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18319.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 5; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1076
ID AAG42684 standard; protein; 465 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53260.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 5; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1077
ID ABB92842 standard; protein; 465 AA.
DE Herbicidially active polypeptide SEQ ID NO 2053.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 5; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1078
ID ADN74399 standard; protein; 465 AA.
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 2294.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDISEIGN NV.
Query Match 5.6%; Score 67; DB 8; Length 465;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1079
ID AAR98835 standard; protein; 472 AA.
DE CD40 associated protein (CDP)-1 clone psk-7 (residues 82-543).
PN WO9616665-A1.
PD 06-JUN-1996.
PA (JOL-) LA JOLLA CANCER RES FOUND.
Query Match 5.6%; Score 67; DB 2; Length 472;
Best Local Similarity 26.2%; Pred. No. 3.3e+02;
RESULT 1080
ID ADD46964 standard; protein; 474 AA.
DE Rat protein Q06000, SEQ ID NO 12650.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;

RESULT 1081
ID ADD48642 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 14348.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1082
ID ADE56912 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 2767.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1083
ID ADE56904 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 2759.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1084
ID ADD46960 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 12646.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1085
ID ADE56908 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 2763.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1086
ID ADD46956 standard; protein; 474 AA.
DE Rat Protein Q06000, SEQ ID NO 12642.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 474;
Best Local Similarity 19.0%; Pred. No. 3.3e+02;
RESULT 1087
ID ADU49562 standard; protein; 484 AA.
DE O11-associated gene related protein #1062.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR) LAURIE C C.
PA (RAVA) RAVANELLO M.
PA (LEDE) LEDEAUX J R.
PA (ROGE) ROGERS J A.
Query Match 5.6%; Score 67; DB 8; Length 484;
Best Local Similarity 23.1%; Pred. No. 3.4e+02;
RESULT 1088
ID AAG17337 standard; protein; 487 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18318.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 67; DB 3; Length 487;
Best Local Similarity 21.6%; Pred. No. 3.4e+02;

RESULT 1089
ID AAG22683 standard; protein; 487 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53259.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.6%; Score 67; DB 3; Length 487;
Best Local Similarity 21.6%; Pred. No. 3.4e+02;
RESULT 1090
ID AAW27434 standard; protein; 512 AA.
DE Human CRAPI isoform p55del9.10.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 512;
Best Local Similarity 26.2%; Pred. No. 3.7e+02;
RESULT 1091
ID AAW27436 standard; protein; 516 AA.
DE Human CRAPI-b isoform p70del8.9.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 516;
Best Local Similarity 26.2%; Pred. No. 3.7e+02;
RESULT 1092
ID AAR98833 standard; protein; 543 AA.
DE CD40 associated protein (C4P)-1.
PN WO9616665-A1.
PD 06-JUN-1996.
PA (LOJL-) LA JOLLA CANCER RES FOUND.
Query Match 5.6%; Score 67; DB 2; Length 543;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 1093
ID AAW27432 standard; protein; 543 AA.
DE Human CRAPI isoform p55del9.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 543;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 1094
ID ABO07169 standard; protein; 543 AA.
DE Human p53 modifying protein, SEQ ID 129.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.6%; Score 67; DB 6; Length 543;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 1095
ID ADQ39697 standard; protein; 543 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1360.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.6%; Score 67; DB 8; Length 543;
Best Local Similarity 26.2%; Pred. No. 4e+02;
RESULT 1096
ID AAR90620 standard; protein; 556 AA.
DE Sulfolobus acidocaldarius amylase for alpha, alpha-trehalose prodn.
PN WO9534642-A1.
PD 21-DEC-1995.
PA (KIRI) KIRIN BEER KK.
Query Match 5.6%; Score 67; DB 2; Length 556;
Best Local Similarity 21.3%; Pred. No. 4.1e+02;
RESULT 1097
ID AAR92755 standard; protein; 556 AA.
DE Trehalose-releasing thermostable enzyme.
PN AU9527131-A.
PD 01-FEB-1996.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
Query Match 5.6%; Score 67; DB 2; Length 556;
Best Local Similarity 21.3%; Pred. No. 4.1e+02;
RESULT 1098
ID AAB67615 standard; protein; 567 AA.

DE Amino acid sequence of human CD40 ligand.
PN WO200116180-A2.
PD 08-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 5.6%; Score 67; DB 4; Length 567;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1099
ID AAO17756 standard; protein; 567 AA.
DE Murine CD40 receptor-associated factor 1 (CRAF1).
PN US2002031522-A1.
PD 14-MAR-2002.
PA (BALT/) BALTIMORE D.
PA (CHEN/) CHENG G.
PA (YEZ/) YE Z.
PA (LEDE/) LEDERMAN S.
PA (CLEA/) CLEARY A.
Query Match 5.6%; Score 67; DB 5; Length 567;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1100
ID ABB57054 standard; protein; 567 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:98.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UNNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 5.6%; Score 67; DB 5; Length 567;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1101
ID ADD25542 standard; protein; 567 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #48.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 5.6%; Score 67; DB 7; Length 567;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1102
ID AAW03146 standard; protein; 568 AA.
DE LMP1 associated protein LAP1.
PN WO9620723-A1.
PD 11-JUL-1996.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.6%; Score 67; DB 2; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1103
ID AAW27431 standard; protein; 568 AA.
DE Human CRAF1-a (TRAF-3-p55) polypeptide.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1104
ID AAY98166 standard; protein; 568 AA.
DE Human TRAF3 protein sequence.
PN WO200020435-A1.
PD 13-APR-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 5.6%; Score 67; DB 3; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1105
ID AAO17757 standard; protein; 568 AA.
DE Human CD40 receptor-associated factor 1 (CRAF1).
PN US2002031522-A1.
PD 14-MAR-2002.
PA (BALT/) BALTIMORE D.
PA (CHEN/) CHENG G.
PA (YEZ/) YE Z.
PA (LEDE/) LEDERMAN S.
PA (CLEA/) CLEARY A.
Query Match 5.6%; Score 67; DB 5; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1106
ID ABO07171 standard; protein; 568 AA.

DE Human p53 modifying protein, SEQ ID 131.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.6%; Score 67; DB 6; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1107
ID ADB80964 standard; protein; 568 AA.
DE RING-SH complex related protein, SEQ ID NO 38.
PN WO2003033646-A2.
PD 24-APR-2003.
PA (PROT-) PROTEOLOGICS INC.
Query Match 5.6%; Score 67; DB 7; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1108
ID ADB80957 standard; protein; 568 AA.
DE RING-SH complex related protein, SEQ ID NO 31.
PN WO2003033646-A2.
PD 24-APR-2003.
PA (PROT-) PROTEOLOGICS INC.
Query Match 5.6%; Score 67; DB 7; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1109
ID ADS88364 standard; protein; 568 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 219.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 67; DB 8; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1110
ID ADQ39695 standard; protein; 568 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1358.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.6%; Score 67; DB 8; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1111
ID ADQ39696 standard; protein; 568 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1359.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.6%; Score 67; DB 8; Length 568;
Best Local Similarity 26.2%; Pred. No. 4.2e+02;
RESULT 1112
ID AAW27435 standard; protein; 634 AA.
DE Human CRAF1-b isoform p70del9,10.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 634;
Best Local Similarity 26.2%; Pred. No. 4.3e+02;
RESULT 1113
ID AAW27437 standard; protein; 638 AA.
DE Human CRAF1-b isoform p70del8,9.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 638;
Best Local Similarity 26.2%; Pred. No. 5e+02;
RESULT 1114
ID AAW27433 standard; protein; 665 AA.
DE Human CRAF1-b isoform p70del9.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 665;
Best Local Similarity 26.2%; Pred. No. 5.3e+02;
RESULT 1115
ID ABR56765 standard; protein; 667 AA.
DE Human secreted protein SECP-40 SEQ ID NO:40.

PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.6%; Score 67; DB 6; Length 667;
Best Local Similarity 19.0%; Pred. No. 5.3e+02;
RESULT 1116
ID ABP54948 standard; protein; 678 AA.
DE Schizosaccharomyces pombe protein kinase Mph1.
PN WO200268444-A1.
PD 06-SEP-2002.
PA (CHIR) CHIRON CORP.
Query Match 5.6%; Score 67; DB 5; Length 678;
Best Local Similarity 22.5%; Pred. No. 5.4e+02;
RESULT 1117
ID ABU61621 standard; protein; 678 AA.
DE Yeast MPH1 protein.
PN US2003045491-A1.
PD 06-MAR-2003.
PA (REIN/) REINHARD C. B.
PA (JEFF/) JEFFERSON A. B.
PA (CHAN/) CHAN V. W.
Query Match 5.6%; Score 67; DB 7; Length 678;
Best Local Similarity 22.5%; Pred. No. 5.4e+02;
RESULT 1118
ID AAM7428 standard; protein; 690 AA.
DE Human CRAF1-b (TRAF-3-p70) polypeptide.
PN WO9734473-A1.
PD 25-SEP-1997.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.6%; Score 67; DB 2; Length 690;
Best Local Similarity 26.2%; Pred. No. 5.5e+02;
RESULT 1119
ID AAB93312 standard; protein; 732 AA.
DE Human protein sequence SEQ ID NO:12391.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.6%; Score 67; DB 4; Length 732;
Best Local Similarity 19.0%; Pred. No. 6e+02;
RESULT 1120
ID ADE56440 standard; protein; 737 AA.
DE Human Protein Q9NY33, SEQ ID NO 2293.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 737;
Best Local Similarity 20.5%; Pred. No. 6e+02;
RESULT 1121
ID ADD45348 standard; protein; 737 AA.
DE Human Protein Q9NY33, SEQ ID NO 10781.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.6%; Score 67; DB 7; Length 737;
Best Local Similarity 20.5%; Pred. No. 6e+02;
RESULT 1122
ID ADO20067 standard; protein; 737 AA.
DE Human PRO polypeptide #488.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 737;
Best Local Similarity 20.5%; Pred. No. 6e+02;
RESULT 1123
ID ADR9354 standard; protein; 753 AA.
DE Human protein useful for treating neurological disease Seq 2860.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.6%; Score 67; DB 8; Length 753;
Best Local Similarity 23.6%; Pred. No. 6.2e+02;

RESULT 1124
ID ADM05476 standard; protein; 804 AA.
DE Human protein of the invention SEQ ID NO:4161.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.6%; Score 67; DB 7; Length 804;
Best Local Similarity 20.3%; Pred. No. 6.8e+02;
RESULT 1125
ID ABU41753 standard; protein; 814 AA.
DE Protein encoded by Prokaryotic essential gene #27280.
PN WO200272783-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 67; DB 6; Length 814;
Best Local Similarity 21.7%; Pred. No. 6.9e+02;
RESULT 1126
ID ADF28113 standard; protein; 815 AA.
DE Murine glycosyl-phosphatidyl-inositol-anchored protein homologue.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 7; Length 815;
Best Local Similarity 23.2%; Pred. No. 6.9e+02;
RESULT 1127
ID AAM79318 standard; protein; 817 AA.
DE Human protein SEQ ID NO 2964.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 817;
Best Local Similarity 23.2%; Pred. No. 7e+02;
RESULT 1128
ID AAM79319 standard; protein; 817 AA.
DE Human protein SEQ ID NO 2965.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 817;
Best Local Similarity 23.2%; Pred. No. 7e+02;
RESULT 1129
ID ABG17558 standard; protein; 885 AA.
DE Novel human diagnostic protein #17549.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 885;
Best Local Similarity 26.1%; Pred. No. 7.8e+02;
RESULT 1130
ID ADP22968 standard; protein; 1181 AA.
DE PRO polypeptide SEQ ID NO:62.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 67; DB 8; Length 1181;
Best Local Similarity 21.3%; Pred. No. 1.2e+03;
RESULT 1131
ID ADC31455 standard; protein; 1216 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1537.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 7; Length 1216;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1132
ID ABM84694 standard; protein; 1242 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4943.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.6%; Score 67; DB 8; Length 1242;
Best Local Similarity 22.9%; Pred. No. 1.2e+03;
RESULT 1133

ID ABG13667 standard; protein; 1682 AA.
DE Novel human diagnostic protein #13658.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 1682;
Best Local Similarity 21.3%; Pred. No. 1.9e+03;
RESULT 1134
ID ABG07239 standard; protein; 1682 AA.
DE Novel human diagnostic protein #7230.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 1682;
Best Local Similarity 21.3%; Pred. No. 1.9e+03;
RESULT 1135
ID ABG19121 standard; protein; 1883 AA.
DE Novel human diagnostic protein #19112.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 1883;
Best Local Similarity 27.4%; Pred. No. 2.2e+03;
RESULT 1136
ID ABG12556 standard; protein; 2002 AA.
DE Novel human diagnostic protein #12547.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 67; DB 4; Length 2002;
Best Local Similarity 27.4%; Pred. No. 2.4e+03;
RESULT 1137
ID ADJ68907 standard; protein; 2294 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID173.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INSTR AGE RES.
Query Match 5.6%; Score 67; DB 7; Length 2294;
Best Local Similarity 25.6%; Pred. No. 2.9e+03;
RESULT 1138
ID ABU33748 standard; protein; 2552 AA.
DE Protein encoded by Prokaryotic essential gene #19275.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 67; DB 6; Length 2552;
Best Local Similarity 21.3%; Pred. No. 3.3e+03;
RESULT 1139
ID AAO23186 standard; protein; 180 AA.
DE Dye-dideoxynucleotide-selected JDP-3 mutant polymerase 12 res 481-660.
PN WO2003054139-A2.
PD 03-JUL-2003.
PA (STRA-) STRATAGENE.
Query Match 5.5%; Score 66.5; DB 7; Length 180;
Best Local Similarity 21.1%; Pred. No. 1e+02;
RESULT 1140
ID ABF53614 standard; protein; 199 AA.
DE Myo-inositol oxygenase amino acid sequence SEQ ID NO:30.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.5%; Score 66.5; DB 5; Length 199;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1141
ID ABF53615 standard; protein; 202 AA.
DE Myo-inositol oxygenase amino acid sequence SEQ ID NO:31.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.5%; Score 66.5; DB 5; Length 202;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1142

ID AAM78514 standard; protein; 210 AA.
DE Human protein SEQ ID NO 1176.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66.5; DB 4; Length 210;
Best Local Similarity 20.1%; Pred. No. 1.2e+02;
RESULT 1143
ID ABP53611 standard; protein; 236 AA.
DE Myo-inositol oxygenase amino acid sequence SEQ ID NO:27.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.5%; Score 66.5; DB 5; Length 236;
Best Local Similarity 22.8%; Pred. No. 1.4e+02;
RESULT 1144
ID ABP53610 standard; protein; 236 AA.
DE Myo-inositol oxygenase amino acid sequence SEQ ID NO:26.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.5%; Score 66.5; DB 5; Length 236;
Best Local Similarity 22.8%; Pred. No. 1.4e+02;
RESULT 1145
ID AAM41606 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6537.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66.5; DB 4; Length 238;
Best Local Similarity 22.8%; Pred. No. 1.5e+02;
RESULT 1146
ID ADL23055 standard; protein; 238 AA.
DE Humanised anti-MAG antibody #2.
PN WO2004014953-A2.
PD 19-FEB-2004.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.5%; Score 66.5; DB 8; Length 238;
Best Local Similarity 23.0%; Pred. No. 1.5e+02;
RESULT 1147
ID ADS88604 standard; protein; 238 AA.
DE Humanised anti-MAG antibody light chain.
PN WO2004083363-A2.
PD 30-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.5%; Score 66.5; DB 8; Length 238;
Best Local Similarity 23.0%; Pred. No. 1.5e+02;
RESULT 1148
ID AAM39820 standard; protein; 239 AA.
DE Human polypeptide SEQ ID NO 2965.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66.5; DB 4; Length 239;
Best Local Similarity 22.8%; Pred. No. 1.5e+02;
RESULT 1149
ID AAY94745 standard; protein; 269 AA.
DE Murine CD8 and human CLA3 fusion protein.
PN WO200056764-A1.
PD 28-SEP-2000.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.5%; Score 66.5; DB 3; Length 269;
Best Local Similarity 23.7%; Pred. No. 1.7e+02;
RESULT 1150
ID ABG17245 standard; protein; 284 AA.
DE Novel human diagnostic protein #17236.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66.5; DB 4; Length 284;
Best Local Similarity 21.2%; Pred. No. 1.9e+02;
RESULT 1151
ID ADP59550 standard; protein; 284 AA.

DE Human polypeptide sequence SEQ ID NO:1958.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66.5; DB 7; Length 284;
Best Local Similarity 21.2%; Pred. No. 1.9e+02;
RESULT 1152
ID AAY58646 standard; protein; 285 AA.
DE Human kidney-specific protein KK86.
PN WO9964435-A1.
PD 16-DEC-1999.
PA (SMTK) SMITHLINE BECHAM CORP.
Query Match 5.5%; Score 66.5; DB 3; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.9e+02;
RESULT 1153
ID AAY5680 standard; protein; 285 AA.
DE Human kidney disease associated protein SEQ ID 12.
PN WO20061622-A2.
PD 19-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.5%; Score 66.5; DB 3; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.9e+02;
RESULT 1154
ID ABP53602 standard; protein; 310 AA.
DE Human myo-inositol oxygenase construct SEQ ID NO:12.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.5%; Score 66.5; DB 5; Length 310;
Best Local Similarity 22.8%; Pred. No. 2.1e+02;
RESULT 1155
ID AAU03104 standard; protein; 321 AA.
DE Thermococcus DNA polymerase JDF-3 mutant 55, fragment.
PN WO200132887-A1.
PD 10-MAY-2001.
PA (STRA-) STRATAGENE.
Query Match 5.5%; Score 66.5; DB 4; Length 321;
Best Local Similarity 21.1%; Pred. No. 2.2e+02;
RESULT 1156
ID AAY94744 standard; protein; 328 AA.
DE Murine CD8 and human CLX5 fusion protein.
PN WO200056764-A1.
PD 28-SEP-2000.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.5%; Score 66.5; DB 3; Length 328;
Best Local Similarity 23.7%; Pred. No. 2.3e+02;
RESULT 1157
ID ABP28638 standard; protein; 328 AA.
DE Streptococcus polypeptide SEQ ID NO 6452.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.5%; Score 66.5; DB 5; Length 328;
Best Local Similarity 34.9%; Pred. No. 2.3e+02;
RESULT 1158
ID ABP28639 standard; protein; 328 AA.
DE Streptococcus polypeptide SEQ ID NO 6454.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.5%; Score 66.5; DB 5; Length 328;
Best Local Similarity 34.9%; Pred. No. 2.3e+02;
RESULT 1159
ID ABU46600 standard; protein; 328 AA.
DE Protein encoded by Prokaryotic essential gene #32127.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66.5; DB 6; Length 328;
Best Local Similarity 34.9%; Pred. No. 2.3e+02;
RESULT 1160

ID AAY94743 standard; protein; 331 AA.
DE Murine CD8 and human CLX18 fusion protein.
PN WO200056764-A1.
PD 28-SEP-2000.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.5%; Score 66.5; DB 3; Length 331;
Best Local Similarity 23.7%; Pred. No. 2.3e+02;
RESULT 1161
ID AAB87443 standard; protein; 347 AA.
DE Human gene 35 encoded secreted protein fragment, SEQ ID NO:184.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 66.5; DB 4; Length 347;
Best Local Similarity 26.4%; Pred. No. 2.5e+02;
RESULT 1162
ID AD809367 standard; protein; 362 AA.
DE Human protein useful for treating neurological disease Seq 2873.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.5%; Score 66.5; DB 8; Length 362;
Best Local Similarity 23.6%; Pred. No. 2.6e+02;
RESULT 1163
ID ABO63696 standard; protein; 398 AA.
DE Klebsiella pneumoniae polypeptide seqid 10213.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66.5; DB 7; Length 398;
Best Local Similarity 21.9%; Pred. No. 3e+02;
RESULT 1164
ID ABP96582 standard; protein; 426 AA.
DE Cow IGF heavy chain amino acid sequence SEQ ID NO:27.
PN WO2003015716-A2.
PD 27-FEB-2003.
PA (IGET-) IGE THERAPEUTICS INC.
Query Match 5.5%; Score 66.5; DB 6; Length 426;
Best Local Similarity 17.2%; Pred. No. 3.2e+02;
RESULT 1165
ID AAG53567 standard; protein; 429 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68239.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 66.5; DB 3; Length 429;
Best Local Similarity 20.8%; Pred. No. 3.3e+02;
RESULT 1166
ID AAG53566 standard; protein; 433 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68238.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 66.5; DB 3; Length 433;
Best Local Similarity 20.8%; Pred. No. 3.3e+02;
RESULT 1167
ID AAB95609 standard; protein; 439 AA.
DE Human protein sequence SEQ ID NO:18311.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66.5; DB 4; Length 439;
Best Local Similarity 26.4%; Pred. No. 3.4e+02;
RESULT 1168
ID AAB80391 standard; protein; 439 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80921, SEQ:969.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERTH) GENEYTECH INC.
Query Match 5.5%; Score 66.5; DB 8; Length 439;
Best Local Similarity 26.4%; Pred. No. 3.4e+02;
RESULT 1169
ID AAY01520 standard; protein; 451 AA.
DE Chicken C-11 protein.
PN JP11075871-A.

PD 23-MAR-1999.
PA (CHUS) CHUGAI PHARM CO LTD.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 5.5%; Score 66.5; DB 2; Length 451;
BEST LOCAL SIMILARITY 22.9%; Pred. NO. 3.5e+02;
RESULT 1170
ID ADG10496 standard; protein; 459 AA.
DE Human STAT6-activating protein, SEQ ID NO:86.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 5.5%; Score 66.5; DB 7; Length 459;
BEST LOCAL SIMILARITY 26.4%; Pred. NO. 3.6e+02;
RESULT 1171
ID ADG10875 standard; protein; 459 AA.
DE Human therapeutic protein - SEQ ID 1112.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NIVE-) NIVELO INC.
Query Match 5.5%; Score 66.5; DB 8; Length 459;
BEST LOCAL SIMILARITY 26.4%; Pred. NO. 3.6e+02;
RESULT 1172
ID ADG12123 standard; protein; 465 AA.
DE Human therapeutic contig protein - SEQ ID 2360.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NIVE-) NIVELO INC.
Query Match 5.5%; Score 66.5; DB 8; Length 465;
BEST LOCAL SIMILARITY 26.4%; Pred. NO. 3.7e+02;
RESULT 1173
ID ABO79462 standard; protein; 514 AA.
DE Pseudomonas aeruginosa polypeptide #11637.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66.5; DB 7; Length 514;
BEST LOCAL SIMILARITY 26.5%; Pred. NO. 4.2e+02;
RESULT 1174
ID ABO83460 standard; protein; 660 AA.
DE Pseudomonas aeruginosa polypeptide #15635.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66.5; DB 7; Length 660;
BEST LOCAL SIMILARITY 23.6%; Pred. NO. 5.9e+02;
RESULT 1175
ID AAY38831 standard; protein; 725 AA.
DE Neisseria meningitidis antigen encoded by ORF23.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.5%; Score 66.5; DB 2; Length 725;
BEST LOCAL SIMILARITY 21.7%; Pred. NO. 6.7e+02;
RESULT 1176
ID ABG33178 standard; protein; 789 AA.
DE Protein encoded by Prokaryotic essential gene #18705.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66.5; DB 6; Length 789;
BEST LOCAL SIMILARITY 25.9%; Pred. NO. 7.6e+02;
RESULT 1177
ID ABB82763 standard; protein; 956 AA.
DE Human CYLD polypeptide.
PN WO200292761-A2.
PD 21-NOV-2002.
PA (IMMV-) IMMUNEX CORP.
Query Match 5.5%; Score 66.5; DB 6; Length 956;
BEST LOCAL SIMILARITY 22.1%; Pred. NO. 9.8e+02;
RESULT 1178
ID ADO95920 standard; protein; 956 AA.
DE T cell activation associated protein #49.
PN WO2004058805-A2.

PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.5%; Score 66.5; DB 8; Length 956;
BEST LOCAL SIMILARITY 22.1%; Pred. NO. 9.8e+02;
RESULT 1179
ID ADR14489 standard; protein; 956 AA.
DE Human NF-kappaB pathway-associated protein SegID490.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 5.5%; Score 66.5; DB 8; Length 956;
BEST LOCAL SIMILARITY 22.1%; Pred. NO. 9.8e+02;
RESULT 1180
ID ABO80673 standard; protein; 1008 AA.
DE Pseudomonas aeruginosa polypeptide #12848.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66.5; DB 7; Length 1008;
BEST LOCAL SIMILARITY 26.2%; Pred. NO. 1.1e+03;
RESULT 1181
ID AAB41592 standard; protein; 2096 AA.
DE Human ORF1356 polypeptide sequence SEQ ID NO:2712.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.5%; Score 66.5; DB 3; Length 2096;
BEST LOCAL SIMILARITY 21.6%; Pred. NO. 2.9e+03;
RESULT 1182
ID ADU76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 5.5%; Score 66.5; DB 8; Length 2397;
BEST LOCAL SIMILARITY 20.0%; Pred. NO. 3.5e+03;
RESULT 1183
ID ABU40513 standard; protein; 129 AA.
DE Protein encoded by Prokaryotic essential gene #26040.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66; DB 6; Length 129;
BEST LOCAL SIMILARITY 26.6%; Pred. NO. 72;
RESULT 1184
ID AAG41898 standard; protein; 152 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52186.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 66; DB 3; Length 152;
BEST LOCAL SIMILARITY 22.8%; Pred. NO. 90;
RESULT 1185
ID AAG25841 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 30068.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 66; DB 3; Length 163;
BEST LOCAL SIMILARITY 22.9%; Pred. NO. 99;
RESULT 1186
ID ABO59731 standard; protein; 185 AA.
DE Human genome derived single exon protein #5965.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANNZ/) HANZEL D K.
Query Match 5.5%; Score 66; DB 8; Length 185;
BEST LOCAL SIMILARITY 23.9%; Pred. NO. 1.2e+02;
RESULT 1187
ID AAG41897 standard; protein; 186 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52185.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 5.5%; Score 66; DB 3; Length 186;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1188
ID ABPE0711 standard; protein; 186 AA.
DE Arabidopsis thaliana thoredoxin M-type 2 SEQ ID NO:60.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 66; DB 5; Length 186;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1189
ID ABO84024 standard; protein; 233 AA.
DE Pseudomonas aeruginosa polypeptide #16199.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66; DB 7; Length 233;
Best Local Similarity 24.5%; Pred. No. 1.6e+02;
RESULT 1190
ID ABG91559 standard; protein; 256 AA.
DE Purine/pyrimidine triphosphate type nucleotidyltransferase #144.
PN WO200248331-A2.
PD 20-JUN-2002.
PA (SLOK-) SLOAN KETTERING INST CANCER RES.
Query Match 5.5%; Score 66; DB 5; Length 256;
Best Local Similarity 24.3%; Pred. No. 1.8e+02;
RESULT 1191
ID ADC97586 standard; protein; 277 AA.
DE E. faecium protein sequence SEQ ID 7213.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66; DB 7; Length 277;
Best Local Similarity 23.9%; Pred. No. 2.1e+02;
RESULT 1192
ID AAB67329 standard; protein; 296 AA.
DE Human neuron progenitor cell clone #1 protein.
PN WO200107607-A2.
PD 01-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66; DB 4; Length 296;
Best Local Similarity 26.3%; Pred. No. 2.2e+02;
RESULT 1193
ID AAE14786 standard; protein; 333 AA.
DE Human immunoglobulin superfamily protein (IGSFP)-6.
PN WO200240671-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 5; Length 333;
Best Local Similarity 22.3%; Pred. No. 2.6e+02;
RESULT 1194
ID ABU0420 standard; protein; 361 AA.
DE Protein encoded by Prokaryotic essential gene #5947.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66; DB 6; Length 361;
Best Local Similarity 23.0%; Pred. No. 3e+02;
RESULT 1195
ID ADB08611 standard; protein; 378 AA.
DE Novel protein (useful for identifying genetic disorders) #766.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 7; Length 378;
Best Local Similarity 26.9%; Pred. No. 3.1e+02;
RESULT 1196
ID ADE09970 standard; protein; 378 AA.
DE Novel protein-related contig polypeptide sequence #558.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.

Query Match 5.5%; Score 66; DB 7; Length 378;
Best Local Similarity 26.9%; Pred. No. 3.1e+02;
RESULT 1197
ID ABG21902 standard; protein; 382 AA.
DE Novel human diagnostic protein #21893.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 4; Length 382;
Best Local Similarity 20.6%; Pred. No. 3.2e+02;
RESULT 1198
ID AAB30535 standard; protein; 405 AA.
DE Fruit fly gustatory receptor protein, Gr36B1.
PN WO200268593-A2.
PD 06-SEP-2002.
PA (UYCO-) UNIV COLUMBIA NEW YORK.
Query Match 5.5%; Score 66; DB 5; Length 405;
Best Local Similarity 28.6%; Pred. No. 3.5e+02;
RESULT 1199
ID AAB85358 standard; protein; 440 AA.
DE Human phosphatase (PP) (clone ID 1723447CD1).
PN WO200153469-A2.
PD 26-JUL-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 4; Length 440;
Best Local Similarity 21.2%; Pred. No. 3.9e+02;
RESULT 1200
ID AAB94895 standard; protein; 442 AA.
DE Human protein sequence SEQ ID NO:16241.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66; DB 4; Length 442;
Best Local Similarity 23.9%; Pred. No. 3.9e+02;
RESULT 1201
ID ABO69784 standard; protein; 462 AA.
DE Pseudomonas aeruginosa polypeptide #1959.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66; DB 7; Length 462;
Best Local Similarity 32.1%; Pred. No. 4.1e+02;
RESULT 1202
ID AAO15421 standard; protein; 471 AA.
DE Human genseet metabolic gene (GMS-7B) protein.
PN WO200255694-A2.
PD 18-JUL-2002.
PA (GRST-) GENSET.
Query Match 5.5%; Score 66; DB 5; Length 471;
Best Local Similarity 23.9%; Pred. No. 4.3e+02;
RESULT 1203
ID AAG23807 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27250.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.5%; Score 66; DB 3; Length 474;
Best Local Similarity 22.9%; Pred. No. 4.3e+02;
RESULT 1204
ID AAB95719 standard; protein; 476 AA.
DE Human protein sequence SEQ ID NO:18587.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66; DB 4; Length 476;
Best Local Similarity 22.4%; Pred. No. 4.3e+02;
RESULT 1205
ID ABR45205 standard; protein; 485 AA.
DE Protein encoded by Prokaryotic essential gene #30732.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66; DB 6; Length 485;
Best Local Similarity 23.1%; Pred. No. 4.4e+02;

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RESULT 1206
ID AAG23806 standard; protein; 493 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27249.
PN EPI033405-A2.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 22.9%; Pred. No. 4.5e+02;
Score 66; DB 3; Length 493;
RESULT 1207
ID ABB58784 standard; protein; 505 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3144.
PN WO200171042-A2.
PD 27-FEB-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 21.4%; Pred. No. 4.7e+02;
Score 66; DB 4; Length 505;
RESULT 1208
ID ABG14307 standard; protein; 517 AA.
DE Novel human diagnostic protein #14298.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 19.9%; Pred. No. 4.8e+02;
Score 66; DB 4; Length 517;
RESULT 1209
ID ABG26147 standard; protein; 523 AA.
DE Novel human diagnostic protein #26138.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 25.0%; Pred. No. 4.9e+02;
Score 66; DB 4; Length 523;
RESULT 1210
ID ABG00694 standard; protein; 524 AA.
DE Novel human diagnostic protein #685.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 4.9e+02;
Score 66; DB 4; Length 524;
RESULT 1211
ID ABG02795 standard; protein; 524 AA.
DE Novel human diagnostic protein #2786.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 4.9e+02;
Score 66; DB 4; Length 524;
RESULT 1212
ID ADI21621 standard; protein; 524 AA.
DE Novel human polypeptide #100.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 4.9e+02;
Score 66; DB 7; Length 524;
RESULT 1213
ID AAB95149 standard; protein; 528 AA.
DE Human protein sequence SEQ ID NO:17175.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 18.8%; Pred. No. 5e+02;
Score 66; DB 4; Length 528;
RESULT 1214
ID AAB93653 standard; protein; 544 AA.
DE Human protein sequence SEQ ID NO:13163.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 18.8%; Pred. No. 5.2e+02;
Score 66; DB 4; Length 544;
RESULT 1215
ID AAB95581 standard; protein; 560 AA.
DE Human protein sequence SEQ ID NO:18241.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 19.7%; Pred. No. 5.4e+02;
Score 66; DB 4; Length 560;
RESULT 1216
ID AAB94345 standard; protein; 561 AA.
DE Human protein sequence SEQ ID NO:14855.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 19.0%; Pred. No. 5.4e+02;
Score 66; DB 4; Length 561;
RESULT 1217
ID AAB25525 standard; protein; 580 AA.
DE Aspergillus fumigatus essential gene protein #183.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.2%; Pred. No. 5.7e+02;
Score 66; DB 6; Length 580;
RESULT 1218
ID ABG08671 standard; protein; 608 AA.
DE Novel human diagnostic protein #8662.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 22.0%; Pred. No. 6e+02;
Score 66; DB 4; Length 608;
RESULT 1219
ID ABG99169 standard; protein; 666 AA.
DE Human endogenous retrovirus K(C7) (herV-K(C7)) gag.
PN WO200246477-A2.
PD 13-JUN-2002.
PA (CHIR ) CHIRON CORP.
Query Match
Best Local Similarity 25.6%; Pred. No. 6.8e+02;
Score 66; DB 5; Length 666;
RESULT 1220
ID ADI83893 standard; protein; 666 AA.
DE HERV-K HML-2 subgroup gag wild-type protein.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR ) CHIRON CORP.
Query Match
Best Local Similarity 25.6%; Pred. No. 6.8e+02;
Score 66; DB 8; Length 666;
RESULT 1221
ID ADI83829 standard; protein; 666 AA.
DE HERV-K HML-2 subgroup HERV-K(C7) gag protein.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR ) CHIRON CORP.
Query Match
Best Local Similarity 25.6%; Pred. No. 6.8e+02;
Score 66; DB 8; Length 666;
RESULT 1222
ID ADJ83894 standard; protein; 667 AA.
DE HERV-K HML-2 subgroup gag optimised protein.
PN WO2003106634-A2.
PD 24-DEC-2003.
PA (CHIR ) CHIRON CORP.
Query Match
Best Local Similarity 25.6%; Pred. No. 6.9e+02;
Score 66; DB 8; Length 667;
RESULT 1223
ID ABJ26125 standard; protein; 680 AA.
DE Aspergillus fumigatus essential gene protein #783.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 21.2%; Pred. No. 7e+02;
Score 66; DB 6; Length 680;
RESULT 1224
ID ABB08645 standard; protein; 709 AA.
DE Human pancreatic cancer antigen SEQ ID NO 9.
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PN JP2001340081-A.
PD 11-DEC-2001.
PA (KEIO-) GH KEIO GIJUKU.
Query Match 5.5%; Score 66; DB 5; Length 709;
Best Local Similarity 23.9%; Pred. No. 7.4e+02;
RESULT 1225
ID AAM78335 standard; protein; 710 AA.
DE Human protein SEQ ID NO 997.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 4; Length 710;
Best Local Similarity 23.9%; Pred. No. 7.5e+02;
RESULT 1226
ID AAO15420 standard; protein; 710 AA.
DE Human genest metabolic gene (GMG-7A) protein.
PN WO200255694-A2.
PD 18-JUL-2002.
PA (GEST-) GENSET.
Query Match 5.5%; Score 66; DB 5; Length 710;
Best Local Similarity 23.9%; Pred. No. 7.5e+02;
RESULT 1227
ID ADF28105 standard; protein; 710 AA.
DE Adiponectin-like protein - SED ID 15.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 7; Length 710;
Best Local Similarity 23.9%; Pred. No. 7.5e+02;
RESULT 1228
ID AAY91954 standard; protein; 731 AA.
DE Human cytoskeleton associated protein 9 (CYSKP-9).
PN WO200017355-A2.
PD 30-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.5%; Score 66; DB 3; Length 731;
Best Local Similarity 22.4%; Pred. No. 7.8e+02;
RESULT 1229
ID AAB95828 standard; protein; 731 AA.
DE Human protein sequence SEQ ID NO:18843.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66; DB 4; Length 731;
Best Local Similarity 22.4%; Pred. No. 7.8e+02;
RESULT 1230
ID AAB97192 standard; protein; 737 AA.
DE Novel human protein SEQ ID NO: 460.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 5; Length 737;
Best Local Similarity 20.5%; Pred. No. 7.9e+02;
RESULT 1231
ID ADF76927 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein SeqID 602.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match 5.5%; Score 66; DB 7; Length 737;
Best Local Similarity 20.5%; Pred. No. 7.9e+02;
RESULT 1232
ID ADP55256 standard; protein; 737 AA.
DE Human PRO protein sequence SEQ ID NO:1232.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.5%; Score 66; DB 8; Length 737;
Best Local Similarity 20.5%; Pred. No. 7.9e+02;
RESULT 1233
ID ADP24969 standard; protein; 737 AA.
DE PRO polypeptide SEQ ID NO:2147.
PN WO2004041170-A2.

PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.5%; Score 66; DB 8; Length 737;
Best Local Similarity 20.5%; Pred. No. 7.9e+02;
RESULT 1234
ID ADM43092 standard; protein; 738 AA.
DE Human PLAP.
PN US2003170784-A1.
PD 11-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.5%; Score 66; DB 7; Length 738;
Best Local Similarity 18.8%; Pred. No. 7.9e+02;
RESULT 1235
ID ADH39770 standard; protein; 738 AA.
DE Streptomyces rochei ORF101 protein SEQ ID NO:101.
PN WO2004001039-A1.
PD 31-DEC-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.5%; Score 66; DB 8; Length 738;
Best Local Similarity 23.5%; Pred. No. 7.9e+02;
RESULT 1236
ID AAB09851 standard; protein; 743 AA.
DE Novel human protein (NHP) #17.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 743;
Best Local Similarity 23.9%; Pred. No. 7.9e+02;
RESULT 1237
ID AAY29512 standard; protein; 746 AA.
DE Human lung tumour protein SAL-25 2nd predicted amino acid sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 66; DB 2; Length 746;
Best Local Similarity 23.9%; Pred. No. 8e+02;
RESULT 1238
ID AAB44461 standard; protein; 746 AA.
DE Human lung tumour-specific antigen encoded by cDNA #98.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 66; DB 3; Length 746;
Best Local Similarity 23.9%; Pred. No. 8e+02;
RESULT 1239
ID AAB13802 standard; protein; 746 AA.
DE Human lung tumour-specific protein SAL-25 #2.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 66; DB 4; Length 746;
Best Local Similarity 23.9%; Pred. No. 8e+02;
RESULT 1240
ID ADP66493 standard; protein; 746 AA.
DE Human lung tumour-specific related protein, SEQ ID No 185.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 66; DB 7; Length 746;
Best Local Similarity 23.9%; Pred. No. 8e+02;
RESULT 1241
ID ADH87747 standard; protein; 746 AA.
DE Human lung tumour antigen polypeptide #55.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.5%; Score 66; DB 7; Length 746;
Best Local Similarity 23.9%; Pred. No. 8e+02;
RESULT 1242
ID ADG64508 standard; protein; 775 AA.
DE Family B DNA-dependent DNA polymerase SEQ ID NO:193.
PN EPI350841-A2.
PD 08-OCT-2003.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.5%; Score 66; DB 7; Length 775;
Best Local Similarity 24.2%; Pred. No. 8.4e+02;
RESULT 1243
ID ADNS9954 standard; protein; 775 AA.
DE 90N Thermococcus sp DNA polymerase protein SEQ ID NO:15.
PN WO2004039947-A2.
PD 13-MAY-2004.
PA (STRA-) STRATAGENE.
Query Match 5.5%; Score 66; DB 8; Length 775;
Best Local Similarity 24.2%; Pred. No. 8.4e+02;
RESULT 1244
ID AAE09853 standard; protein; 792 AA.
DE Novel human protein (NHP) #19.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 792;
Best Local Similarity 23.9%; Pred. No. 8.7e+02;
RESULT 1245
ID AAY95968 standard; protein; 795 AA.
DE Human TANGO 243.
PN WO200050443-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.5%; Score 66; DB 3; Length 795;
Best Local Similarity 18.8%; Pred. No. 8.7e+02;
RESULT 1246
ID AAB68514 standard; protein; 795 AA.
DE Human GTP-binding associated protein #14.
PN WO200105970-A2.
PD 25-JAN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 4; Length 795;
Best Local Similarity 18.8%; Pred. No. 8.7e+02;
RESULT 1247
ID AAB93162 standard; protein; 795 AA.
DE Human protein sequence SEQ ID NO:12087.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.5%; Score 66; DB 4; Length 795;
Best Local Similarity 18.8%; Pred. No. 8.7e+02;
RESULT 1248
ID ADM43083 standard; protein; 795 AA.
DE Human TANGO 243.
PN US2003170784-A1.
PD 11-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.5%; Score 66; DB 7; Length 795;
Best Local Similarity 18.8%; Pred. No. 8.7e+02;
RESULT 1249
ID AAM78334 standard; protein; 800 AA.
DE Human protein SEQ ID NO 996.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 4; Length 800;
Best Local Similarity 23.9%; Pred. No. 8.8e+02;
RESULT 1250
ID ADP28095 standard; protein; 800 AA.
DE Adiponectin-like protein - SED ID 5.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 7; Length 800;
Best Local Similarity 23.9%; Pred. No. 8.8e+02;
RESULT 1251
ID ADA20755 standard; protein; 809 AA.
DE Soybean phospholipase D alpha #2.
PN US2003003471-A1.
PD 02-JAN-2003.

PA (FAMO/) FAMODU O O.
PA (MIAO/) MIAO G.
PA (SIMM/) SIMMONS C R.
PA (WENG/) WENG Z.
PA (CAHO/) CAHOON R E.
PA (SAKA/) SAKAI H.
PA (QUINZ/) QUN Z.
PA (THOR/) THORPE C J.
PA (FADE/) FADER G M.
PA (LIBB/) LI B.
Query Match 5.5%; Score 66; DB 6; Length 809;
Best Local Similarity 22.8%; Pred. No. 8.9e+02;
RESULT 1252
ID ABR43183 standard; protein; 821 AA.
DE Human REMAP-15 protein SEQ ID NO:15.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 6; Length 821;
Best Local Similarity 23.9%; Pred. No. 9.1e+02;
RESULT 1253
ID ABR92061 standard; protein; 824 AA.
DE Human receptors and membrane associated protein REMAP-4.
PN WO200263006-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 5; Length 824;
Best Local Similarity 23.9%; Pred. No. 9.2e+02;
RESULT 1254
ID AAE09855 standard; protein; 827 AA.
DE Novel human protein (NHP) #21.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 827;
Best Local Similarity 23.9%; Pred. No. 9.2e+02;
RESULT 1255
ID ABR43200 standard; protein; 844 AA.
DE Human REMAP-32 protein SEQ ID NO:32.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 6; Length 844;
Best Local Similarity 23.9%; Pred. No. 9.5e+02;
RESULT 1256
ID AAY95969 standard; protein; 855 AA.
DE Human TANGO 243 (alternative translation).
PN WO200050443-A2.
PD 31-AUG-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.5%; Score 66; DB 3; Length 855;
Best Local Similarity 18.8%; Pred. No. 9.6e+02;
RESULT 1257
ID ADM43107 standard; protein; 855 AA.
DE Human TANGO 243 long form.
PN US2003170784-A1.
PD 11-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.5%; Score 66; DB 7; Length 855;
Best Local Similarity 18.8%; Pred. No. 9.6e+02;
RESULT 1258
ID ADC31681 standard; protein; 863 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1763.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 7; Length 863;
Best Local Similarity 19.7%; Pred. No. 9.8e+02;
RESULT 1259
ID AAE09850 standard; protein; 877 AA.
DE Novel human protein (NHP) #16.
PN WO200164718-A2.
PD 07-SEP-2001.

PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 877;
Best Local Similarity 23.9%; Pred. No. 1e+03;
RESULT 1260
ID AAB09839 standard; protein; 908 AA.
DE Novel human protein (NHP) #8.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 908;
Best Local Similarity 23.9%; Pred. No. 1e+03;
RESULT 1261
ID AAB09845 standard; protein; 909 AA.
DE Novel human protein (NHP) #11.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 909;
Best Local Similarity 23.9%; Pred. No. 1e+03;
RESULT 1262
ID AAB09852 standard; protein; 926 AA.
DE Novel human protein (NHP) #18.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 926;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1263
ID AAB80172 standard; protein; 944 AA.
DE A. fumigatus AfBGL1.
PN WO2003012071-A2.
PD 13-FEB-2003.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66; DB 6; Length 944;
Best Local Similarity 25.5%; Pred. No. 1.1e+03;
RESULT 1264
ID ADC24816 standard; protein; 953 AA.
DE Human breast specific polypeptide (BSP) DEX0238_137, SEQ ID NO:137.
PN WO2003020900-A2.
PD 13-MAR-2003.
PA (DIDAD-) DIDADXUS INC.
Query Match 5.5%; Score 66; DB 7; Length 953;
Best Local Similarity 22.4%; Pred. No. 1.1e+03;
RESULT 1265
ID ADQ95918 standard; protein; 953 AA.
DE T cell activation associated protein #48.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.5%; Score 66; DB 8; Length 953;
Best Local Similarity 22.4%; Pred. No. 1.1e+03;
RESULT 1266
ID ADQ95916 standard; protein; 953 AA.
DE T cell activation associated protein #47.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.5%; Score 66; DB 8; Length 953;
Best Local Similarity 22.4%; Pred. No. 1.1e+03;
RESULT 1267
ID AAB09841 standard; protein; 957 AA.
DE Novel human protein (NHP) #7.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 957;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1268
ID AAB09847 standard; protein; 958 AA.
DE Novel human protein (NHP) #13.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 5.5%; Score 66; DB 4; Length 958;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1269
ID ADP9244 standard; protein; 960 AA.
DE DKFZP586D1122, SEQ ID 250.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 5.5%; Score 66; DB 8; Length 960;
Best Local Similarity 22.4%; Pred. No. 1.1e+03;
RESULT 1270
ID AAB09854 standard; protein; 961 AA.
DE Novel human protein (NHP) #20.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 961;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1271
ID AAB09843 standard; protein; 992 AA.
DE Novel human protein (NHP) #9.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 992;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1272
ID AAB09849 standard; protein; 993 AA.
DE Novel human protein (NHP) #15.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 993;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1273
ID AAB09838 standard; protein; 1042 AA.
DE Novel human protein (NHP) #4.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1042;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1274
ID ADN20125 standard; protein; 1042 AA.
DE Bacterial polypeptide #2778.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 66; DB 8; Length 1042;
Best Local Similarity 22.3%; Pred. No. 1.1e+03;
RESULT 1275
ID AAB09844 standard; protein; 1043 AA.
DE Novel human protein (NHP) #10.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1043;
Best Local Similarity 23.9%; Pred. No. 1.1e+03;
RESULT 1276
ID ADS28006 standard; protein; 1078 AA.
DE Bacterial polypeptide #17039.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 66; DB 8; Length 1078;

Best Local Similarity 25.8%; Pred. No. 1.3e+03;
RESULT 1277
ID AAB09840 standard; protein; 1091 AA.
DE Novel human protein (NHP) #6.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1091;
Best Local Similarity 23.9%; Pred. No. 1.3e+03;
RESULT 1278
ID AAB09846 standard; protein; 1092 AA.
DE Novel human protein (NHP) #12.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1092;
Best Local Similarity 23.9%; Pred. No. 1.3e+03;
RESULT 1279
ID ABO75628 standard; protein; 1116 AA.
DE Pseudomonas aeruginosa polypeptide #7803.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.5%; Score 66; DB 7; Length 1116;
Best Local Similarity 25.5%; Pred. No. 1.4e+03;
RESULT 1280
ID AAB09842 standard; protein; 1126 AA.
DE Novel human protein (NHP) #8.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1126;
Best Local Similarity 23.9%; Pred. No. 1.4e+03;
RESULT 1281
ID AAB09848 standard; protein; 1127 AA.
DE Novel human protein (NHP) #14.
PN WO200164718-A2.
PD 07-SEP-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.5%; Score 66; DB 4; Length 1127;
Best Local Similarity 23.9%; Pred. No. 1.4e+03;
RESULT 1282
ID ADI43353 standard; protein; 1354 AA.
DE Human intracellular signalling (INTSIG) protein #1.
PN WO2003060064-A2.
PD 24-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.5%; Score 66; DB 7; Length 1354;
Best Local Similarity 19.7%; Pred. No. 1.8e+03;
RESULT 1283
ID ADH88855 standard; protein; 1467 AA.
DE Enterococcus faecalis polypeptide #3335.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.5%; Score 66; DB 7; Length 1467;
Best Local Similarity 22.6%; Pred. No. 2e+03;
RESULT 1284
ID ABU21966 standard; protein; 1632 AA.
DE Protein encoded by Prokaryotic essential gene #7493.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 66; DB 6; Length 1632;
Best Local Similarity 21.1%; Pred. No. 2.3e+03;
RESULT 1285
ID ABG18356 standard; protein; 1641 AA.
DE Novel human diagnostic protein #18347.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 4; Length 1641;

Best Local Similarity 18.9%; Pred. No. 2.4e+03;
RESULT 1286
ID ABB58422 standard; protein; 1713 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2058.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 66; DB 4; Length 1713;
Best Local Similarity 26.0%; Pred. No. 2.5e+03;
RESULT 1287
ID ABG02199 standard; protein; 2012 AA.
DE Novel human diagnostic protein #2190.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 66; DB 4; Length 2012;
Best Local Similarity 22.0%; Pred. No. 3.1e+03;
RESULT 1288
ID AAM08333 standard; protein; 2089 AA.
DE Cycloella cryptica acetyl-coenzyme A carboxylase.
PN US5559220-A.
PD 24-SEP-1996.
PA (MTDE) MIDWEST RES INST.
Query Match 5.5%; Score 66; DB 2; Length 2089;
Best Local Similarity 20.8%; Pred. No. 3.3e+03;
RESULT 1289
ID ABB81068 standard; protein; 2326 AA.
DE Rat NG2 protein.
PN WO200259607-A2.
PD 01-AUG-2002.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 5.5%; Score 66; DB 5; Length 2326;
Best Local Similarity 23.6%; Pred. No. 3.8e+03;
RESULT 1290
ID AD031204 standard; protein; 2326 AA.
DE Rat NG2 protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UVCA-) UNIV CASE WESTERN RESERVE.
Query Match 5.5%; Score 66; DB 8; Length 2326;
Best Local Similarity 23.6%; Pred. No. 3.8e+03;
RESULT 1291
ID AAG57787 standard; protein; 136 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 74510.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 65.5; DB 3; Length 136;
Best Local Similarity 20.4%; Pred. No. 88;
RESULT 1292
ID AAP90731 standard; protein; 195 AA.
DE Limulus polyphemus coagulogen.
PN JP01160484-A.
PD 23-JUN-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 5.4%; Score 65.5; DB 1; Length 195;
Best Local Similarity 20.8%; Pred. No. 1.4e+02;
RESULT 1293
ID ABR53616 standard; protein; 202 AA.
DE Myo-inositol oxygenase amino acid sequence SEQ ID NO:32.
PN WO200274926-A2.
PD 26-SEP-2002.
PA (CRGI) CARGILL INC.
Query Match 5.4%; Score 65.5; DB 5; Length 202;
Best Local Similarity 20.5%; Pred. No. 1.5e+02;
RESULT 1294
ID ADF04359 standard; protein; 214 AA.
DE Bacterial polypeptide #472.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65.5; DB 7; Length 214;
Best Local Similarity 22.0%; Pred. No. 1.6e+02;
RESULT 1295

ID AD007415 standard; protein; 214 AA.
DE Mature CBE11 chimeric light chain antibody construct.
PN WO2004058183-A2.
PD 15-JUL-2004.
PA (BIOGEN) BIOGEN IDEC MA INC.
Query Match 5.4%; Score 65.5; DB 8; Length 214;
Best Local Similarity 22.9%; Pred. No. 1.6e+02;
RESULT 1296
ID ADQ12198 standard; protein; 214 AA.
DE CBE11 pentameric light chain antibody.
PN WO2004058191-A2.
PD 15-JUL-2004.
PA (BIOGEN) BIOGEN IDEC MA INC.
Query Match 5.4%; Score 65.5; DB 8; Length 214;
Best Local Similarity 22.9%; Pred. No. 1.6e+02;
RESULT 1297
ID AAB19182 standard; protein; 218 AA.
DE Human protease. PRS-19 protein.
PN WO200208396-A2.
PD 31-JAN-2002.
PA (INCYTE) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65.5; DB 5; Length 218;
Best Local Similarity 29.9%; Pred. No. 1.7e+02;
RESULT 1298
ID ABG70052 standard; protein; 234 AA.
DE Human prey protein for Shigella ospb #11.
PN WO200257303-A2.
PD 25-JUL-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 5.4%; Score 65.5; DB 5; Length 234;
Best Local Similarity 24.4%; Pred. No. 1.9e+02;
RESULT 1299
ID ADL3649 standard; protein; 238 AA.
DE Human CD44-binding antibody light chain HAE-A3-kappa-light SEQ ID NO:144.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 5.4%; Score 65.5; DB 8; Length 238;
Best Local Similarity 21.5%; Pred. No. 1.9e+02;
RESULT 1300
ID ADS88785 standard; protein; 238 AA.
DE Sequence of the chimeric ICG kappa light chain in M13mp19 clone M609.
PN WO2004083373-A2.
PD 30-SEP-2004.
PA (UYNE-) UNIV NEWCASTLE-UPON-TYNE.
Query Match 5.4%; Score 65.5; DB 8; Length 238;
Best Local Similarity 21.7%; Pred. No. 1.9e+02;
RESULT 1301
ID ABG01661 standard; protein; 264 AA.
DE Novel human diagnostic protein #1652.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65.5; DB 4; Length 264;
Best Local Similarity 22.0%; Pred. No. 2.2e+02;
RESULT 1302
ID AAB10683 standard; protein; 279 AA.
DE C. glutamicum panc protein.
PN DE1907567-A1.
PD 24-AUG-2000.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Query Match 5.4%; Score 65.5; DB 3; Length 279;
Best Local Similarity 26.5%; Pred. No. 2.4e+02;
RESULT 1303
ID AAB10034 standard; protein; 279 AA.
DE C. glutamicum panc protein.
PN EPI006189-A2.
PD 07-JUN-2000.
PA (DEGS) DEGUSSA-HUELS AG.
Query Match 5.4%; Score 65.5; DB 3; Length 279;
Best Local Similarity 26.5%; Pred. No. 2.4e+02;
RESULT 1304

ID AAB10032 standard; protein; 279 AA.
DE C. glutamicum panc protein.
PN EPI006192-A2.
PD 07-JUN-2000.
PA (DEGS) DEGUSSA-HUELS AG.
Query Match 5.4%; Score 65.5; DB 3; Length 279;
Best Local Similarity 26.5%; Pred. No. 2.4e+02;
RESULT 1305
ID AAB79940 standard; protein; 279 AA.
DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:614.
PN WO200100843-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 5.4%; Score 65.5; DB 4; Length 279;
Best Local Similarity 26.5%; Pred. No. 2.4e+02;
RESULT 1306
ID AAG89878 standard; protein; 279 AA.
DE C glutamicum protein fragment SEQ ID NO: 3632.
PN EPI08790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 65.5; DB 4; Length 279;
Best Local Similarity 26.5%; Pred. No. 2.4e+02;
RESULT 1307
ID AAY37026 standard; protein; 282 AA.
DE Chlamydia trachomatis lipoprotein sequence.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GRST) GENSET.
Query Match 5.4%; Score 65.5; DB 2; Length 282;
Best Local Similarity 18.3%; Pred. No. 2.4e+02;
RESULT 1308
ID AAU14730 standard; protein; 353 AA.
DE Novel bone marrow polypeptide #129.
PN WO200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65.5; DB 4; Length 353;
Best Local Similarity 24.4%; Pred. No. 3.3e+02;
RESULT 1309
ID ADN26874 standard; protein; 371 AA.
DE Bacterial polypeptide #9527.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.4%; Score 65.5; DB 8; Length 371;
Best Local Similarity 21.3%; Pred. No. 3.5e+02;
RESULT 1310
ID ABB58017 standard; protein; 372 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 843.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 65.5; DB 4; Length 372;
Best Local Similarity 25.4%; Pred. No. 3.5e+02;
RESULT 1311
ID ABG25330 standard; protein; 373 AA.
DE Novel human diagnostic protein #25321.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65.5; DB 4; Length 373;
Best Local Similarity 28.3%; Pred. No. 3.5e+02;
RESULT 1312
ID ADK13795 standard; protein; 375 AA.
DE E. coli iron transport and metabolism protein SEQ ID NO:90.
PN WO2004018638-A2.
PD 04-MAR-2004.
PA (MINU) UNIV MINNESOTA.

PA (KAPU/) KAPUR V.
PA (GADG/) GADGIL M.
Query Match 5.4%; Score 65.5; DB 8; Length 375;
Best Local Similarity 20.6%; Pred. No. 3.5e+02;
RESULT 1313
ID AAW80937 standard; protein; 379 AA.
DE Human heart lectin-h-cholesterol acyltransferase-like protein 1.
PN WO3846767-A1.
PD 22-OCT-1998.
PA (TAKE) TAKEBA CHEM IND LTD.
Query Match 5.4%; Score 65.5; DB 2; Length 379;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1314
ID ADE25555 standard; protein; 379 AA.
DE Human Lfpl protein SEQ ID NO 1.
PN WO2003062416-A1.
PD 31-JUN-2003.
PA (TAKE) TAKEBA CHEM IND LTD.
Query Match 5.4%; Score 65.5; DB 7; Length 379;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1315
ID ADG14394 standard; protein; 379 AA.
DE Human Lfpl, SEQ ID 8.
PN WO2003078624-A1.
PD 25-SEP-2003.
PA (TAKE) TAKEBA CHEM IND LTD.
Query Match 5.4%; Score 65.5; DB 7; Length 379;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1316
ID AAW80940 standard; protein; 382 AA.
DE Human heart lectin-h-cholesterol acyltransferase-like protein 2.
PN WO3846767-A1.
PD 22-OCT-1998.
PA (TAKE) TAKEBA CHEM IND LTD.
Query Match 5.4%; Score 65.5; DB 2; Length 382;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1317
ID ADG14398 standard; protein; 382 AA.
DE Human Lfpl, SEQ ID 12.
PN WO2003078624-A1.
PD 25-SEP-2003.
PA (TAKE) TAKEBA CHEM IND LTD.
Query Match 5.4%; Score 65.5; DB 7; Length 382;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1318
ID ABM69987 standard; protein; 389 AA.
DE Photorhabdus luminescens protein sequence #3084.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 5.4%; Score 65.5; DB 7; Length 382;
Best Local Similarity 20.6%; Pred. No. 3.6e+02;
RESULT 1319
ID ABB76399 standard; protein; 401 AA.
DE Phaffia rhodozyma alternative oxidase AOX.
PN EP1158051-A1.
PD 28-NOV-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.4%; Score 65.5; DB 5; Length 401;
Best Local Similarity 18.2%; Pred. No. 3.9e+02;
RESULT 1320
ID ADG42973 standard; protein; 409 AA.
DE Bacterial polypeptide #21403.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.4%; Score 65.5; DB 8; Length 409;
Best Local Similarity 25.3%; Pred. No. 4e+02;

RESULT 1321
ID ABO32530 standard; protein; 421 AA.
DE Secreted polypeptide-related protein #16.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS) FRASER C C.
PA (BARN) BARNES T M.
PA (SHAR) SHARP J D.
PA (KIRS) KIRST S J.
PA (MYER) MYERS P S.
PA (LEIB) LEIBY K R.
PA (HOLT) HOLTMAN D A.
PA (WRIK) WRIGHTON N.
PA (MCCA) MCCARTHY S A.
PA (MACK) MACKAY C R.
PA (GOOD) GOODEARL A D J.
Query Match 5.4%; Score 65.5; DB 6; Length 421;
Best Local Similarity 22.0%; Pred. No. 4.2e+02;
RESULT 1322
ID ADQ10139 standard; protein; 421 AA.
DE Human polypeptide #22.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL) MILLENNIUM PHARM INC.
Query Match 5.4%; Score 65.5; DB 8; Length 421;
Best Local Similarity 22.0%; Pred. No. 4.2e+02;
RESULT 1323
ID ABP97603 standard; protein; 427 AA.
DE Amino acid sequence of a NAD+-dependent DNA ligase.
PN WO2003000858-A2.
PD 03-JAN-2003.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.4%; Score 65.5; DB 6; Length 427;
Best Local Similarity 25.0%; Pred. No. 4.2e+02;
RESULT 1324
ID AAG28833 standard; protein; 429 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 65.5; DB 3; Length 429;
Best Local Similarity 20.8%; Pred. No. 4.3e+02;
RESULT 1325
ID AAG28832 standard; protein; 433 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34198.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 65.5; DB 3; Length 433;
Best Local Similarity 20.8%; Pred. No. 4.3e+02;
RESULT 1326
ID ADJ69123 standard; protein; 435 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID929.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.4%; Score 65.5; DB 7; Length 435;
Best Local Similarity 30.5%; Pred. No. 4.3e+02;
RESULT 1327
ID AAB24513 standard; protein; 442 AA.
DE Human secreted protein sequence encoded by gene 12 SEQ ID NO:139.
PN WO2003035937-A1.
PD 22-JUN-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 65.5; DB 3; Length 442;
Best Local Similarity 25.7%; Pred. No. 4.4e+02;
RESULT 1328
ID ADN46391 standard; protein; 450 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID269.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.4%; Score 65.5; DB 8; Length 450;
Best Local Similarity 23.5%; Pred. No. 4.6e+02;

RESULT 1329
ID ABO79970 standard; protein; 454 AA.
DE Pseudomonas aeruginosa polypeptide #12145.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65.5; DB 7; Length 454;
Best Local Similarity 23.7%; Pred. No. 4.6e+02;
RESULT 1330
ID ADR44430 standard; protein; 472 AA.
DE Rat selenium binding protein.
PN US2004170629-A1.
PD 02-SEP-2004.
PA (HAMA/) HAMA/MY M. M.
Query Match 5.4%; Score 65.5; DB 8; Length 472;
Best Local Similarity 23.5%; Pred. No. 4.9e+02;
RESULT 1331
ID AAU00628 standard; protein; 487 AA.
DE Novel human protein (NHP) sequence #1.
PN WO200128219-A1.
PD 26-APR-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65.5; DB 4; Length 487;
Best Local Similarity 22.0%; Pred. No. 5.1e+02;
RESULT 1332
ID ADM04757 standard; protein; 524 AA.
DE Human protein of the invention SEQ ID NO:3442.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.4%; Score 65.5; DB 7; Length 524;
Best Local Similarity 22.0%; Pred. No. 5.6e+02;
RESULT 1333
ID AAU00630 standard; protein; 539 AA.
DE Novel human protein (NHP) sequence #3.
PN WO200129219-A1.
PD 26-APR-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65.5; DB 4; Length 539;
Best Local Similarity 22.0%; Pred. No. 5.8e+02;
RESULT 1334
ID ADN39981 standard; protein; 539 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C351.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.4%; Score 65.5; DB 7; Length 539;
Best Local Similarity 22.0%; Pred. No. 5.8e+02;
RESULT 1335
ID ADR46669 standard; protein; 539 AA.
DE Cancer-associated protein, SEQ ID 82.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.4%; Score 65.5; DB 8; Length 539;
Best Local Similarity 22.0%; Pred. No. 5.8e+02;
RESULT 1336
ID ADR46668 standard; protein; 539 AA.
DE Cancer-associated protein, SEQ ID 81.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.4%; Score 65.5; DB 8; Length 539;
Best Local Similarity 22.0%; Pred. No. 5.8e+02;
RESULT 1337
ID ADB65022 standard; protein; 575 AA.
DE Human protein encoded by clone SKMCM10001230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 5.4%; Score 65.5; DB 7; Length 575;
Best Local Similarity 23.9%; Pred. No. 6.4e+02;

RESULT 1338
ID AAU00629 standard; protein; 586 AA.
DE Novel human protein (NHP) sequence #2.
PN WO200129219-A1.
PD 26-APR-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65.5; DB 4; Length 586;
Best Local Similarity 22.0%; Pred. No. 6.5e+02;
RESULT 1339
ID ADN39982 standard; protein; 586 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C352.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.4%; Score 65.5; DB 7; Length 586;
Best Local Similarity 22.0%; Pred. No. 6.5e+02;
RESULT 1340
ID ADC96778 standard; protein; 587 AA.
DE E. faecium protein sequence SEQ ID 6405.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65.5; DB 7; Length 587;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1341
ID ADS95086 standard; protein; 600 AA.
DE Human therapeutic protein sequence #44, SEQ ID 125.
PN WO2004039319-A2.
PD 13-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.4%; Score 65.5; DB 8; Length 600;
Best Local Similarity 23.9%; Pred. No. 6.8e+02;
RESULT 1342
ID ABG52129 standard; protein; 625 AA.
DE Novel human diagnostic protein #25120.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65.5; DB 4; Length 625;
Best Local Similarity 24.6%; Pred. No. 7.1e+02;
RESULT 1343
ID ADI28019 standard; protein; 641 AA.
DE ECMCAD protein 184661CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65.5; DB 5; Length 641;
Best Local Similarity 22.0%; Pred. No. 7.4e+02;
RESULT 1344
ID ABJ39109 standard; protein; 643 AA.
DE Protein encoded by Prokaryotic essential gene #24636.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.4%; Score 65.5; DB 6; Length 643;
Best Local Similarity 21.7%; Pred. No. 7.4e+02;
RESULT 1345
ID ADS14914 standard; protein; 664 AA.
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 469.
PN WO200408385-A2.
PD 30-SEP-2004.
PA (IOWA) IOWA RES FOUND.
Query Match 5.4%; Score 65.5; DB 8; Length 664;
Best Local Similarity 23.0%; Pred. No. 7.8e+02;
RESULT 1346
ID ABO32529 standard; protein; 681 AA.
DE Secreted polypeptide-related protein #15.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C. C.
PA (BARN/) BARNES T. M.
PA (SHAR/) SHARP J. D.
PA (KIRST/) KIRST S. J.

PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
DE (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODERL A D J.
Query Match 5.4%; Score 65.5; DB 6; Length 681;
Best Local Similarity 22.0%; Pred. No. 8e+02;
RESULT 1347
ID ADQ10138 standard; protein; 681 AA.
DE Human polypeptide #21.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.4%; Score 65.5; DB 8; Length 681;
Best Local Similarity 22.0%; Pred. No. 8e+02;
RESULT 1348
ID ABO76020 standard; protein; 706 AA.
DE Pseudomonas aeruginosa polypeptide #8195.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65.5; DB 7; Length 706;
Best Local Similarity 23.0%; Pred. No. 8.4e+02;
RESULT 1349
ID AAU00670 standard; protein; 715 AA.
DE Human TANGO 229 polypeptide.
PN WO200129088-A1.
PD 26-APR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.4%; Score 65.5; DB 4; Length 715;
Best Local Similarity 22.0%; Pred. No. 8.6e+02;
RESULT 1350
ID ABB81000 standard; protein; 715 AA.
DE Human neutrophilin homologue polypeptide, zcub5.
PN WO200253739-A2.
PD 11-JUL-2002.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match 5.4%; Score 65.5; DB 5; Length 715;
Best Local Similarity 22.0%; Pred. No. 8.6e+02;
RESULT 1351
ID ABO32527 standard; protein; 715 AA.
DE Secreted polypeptide-related protein #14.
PN US2003022379-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODERL A D J.
Query Match 5.4%; Score 65.5; DB 6; Length 715;
Best Local Similarity 22.0%; Pred. No. 8.6e+02;
RESULT 1352
ID ADQ10136 standard; protein; 715 AA.
DE Human polypeptide #19.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.4%; Score 65.5; DB 8; Length 715;
Best Local Similarity 22.0%; Pred. No. 8.6e+02;
RESULT 1353
ID ABO17337 standard; protein; 847 AA.
DE Novel human diagnostic protein #17328.
PN WO20015067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 5.4%; Score 65.5; DB 4; Length 847;
Best Local Similarity 24.4%; Pred. No. 1.1e+03;
RESULT 1354
ID ABG62066 standard; protein; 932 AA.
DE Human tumour suppressor protein #21.
PN WO200226815-A2.
PD 04-APR-2002.
PA (VIAA-) VIAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 5.4%; Score 65.5; DB 5; Length 932;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1355
ID ABR47437 standard; protein; 1101 AA.
DE Breast cancer associated protein sequence SEQ ID NO:106.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.4%; Score 65.5; DB 6; Length 1101;
Best Local Similarity 31.3%; Pred. No. 1.6e+03;
RESULT 1356
ID ADJ70375 standard; protein; 1101 AA.
DE Human heart mitochondrial protein as a therapeutic target SeqID2181.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.4%; Score 65.5; DB 7; Length 1101;
Best Local Similarity 31.3%; Pred. No. 1.6e+03;
RESULT 1357
ID ADQ20338 standard; protein; 1101 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3158.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.4%; Score 65.5; DB 8; Length 1101;
Best Local Similarity 31.3%; Pred. No. 1.6e+03;
RESULT 1358
ID ADM57331 standard; protein; 1265 AA.
DE Recombinant protein production method related polypeptide SEQ ID NO: 12.
PN WO2004027067-A2.
PD 01-APR-2004.
PA (CYMO-) CYMP AS.
Query Match 5.4%; Score 65.5; DB 8; Length 1265;
Best Local Similarity 29.2%; Pred. No. 1.9e+03;
RESULT 1359
ID AAG48316 standard; protein; 1280 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61001.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.4%; Score 65.5; DB 3; Length 1280;
Best Local Similarity 29.2%; Pred. No. 1.9e+03;
RESULT 1360
ID AAE32114 standard; protein; 1360 AA.
DE Human cytoskeleton-associated protein, CSAP-12.
PN WO200279404-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65.5; DB 6; Length 1360;
Best Local Similarity 31.3%; Pred. No. 2.1e+03;
RESULT 1361
ID AAY72711 standard; protein; 1473 AA.
DE Human NAC beta isoform, alternative version.
PN WO200116170-A2.
PD 08-MAR-2001.
PA (BORN-) BORNHAM INST.
Query Match 5.4%; Score 65.5; DB 4; Length 1473;
Best Local Similarity 24.8%; Pred. No. 2.3e+03;
RESULT 1362
ID AAR21179 standard; protein; 1864 AA.
DE Human TRICH-23 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65.5; DB 5; Length 1864;

Best Local Similarity 21.1%; Pred. No. 3.2e+03;
RESULT 1363
ID ABU62065 standard; protein; 1864 AA.
DE Human melanoma alpha-kinase (MK).
PN US2002177205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 5.4%; Score 65.5; DB 6; Length 1864;
Best Local Similarity 21.1%; Pred. No. 3.2e+03;
RESULT 1364
ID AAUS9034 standard; protein; 109 AA.
DE Propionibacterium acnes immunogenic protein #19930.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.4%; Score 65; DB 4; Length 109;
Best Local Similarity 30.0%; Pred. No. 74;
RESULT 1365
ID ABMS5553 standard; protein; 109 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #20229.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.4%; Score 65; DB 6; Length 109;
Best Local Similarity 30.0%; Pred. No. 74;
RESULT 1366
ID AAU66966 standard; protein; 122 AA.
DE Propionibacterium acnes immunogenic protein #27862.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.4%; Score 65; DB 4; Length 122;
Best Local Similarity 30.0%; Pred. No. 87;
RESULT 1367
ID ABMS3485 standard; protein; 122 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28161.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.4%; Score 65; DB 6; Length 122;
Best Local Similarity 30.0%; Pred. No. 87;
RESULT 1368
ID AAES5967 standard; protein; 163 AA.
DE Phosphoinositide-specific phospholipase C domain #1.
PN WO200153326-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 163;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 1369
ID AAO23184 standard; protein; 180 AA.
DE Dye-deoxyxynuclease-selected JDF-3 mutant polymerase 10 res 481-660.
PN WO2003054139-A2.
PD 03-JUL-2003.
PA (STRA-) STRATAGENE.
Query Match 5.4%; Score 65; DB 7; Length 180;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 1370
ID ADNA7561 standard; protein; 197 AA.
DE Thermococcus kodakarensis KOD1 protein sequence SeqID1439.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.4%; Score 65; DB 8; Length 197;
Best Local Similarity 21.8%; Pred. No. 1.7e+02;
RESULT 1371
ID AAY74195 standard; protein; 198 AA.
DE Human prostate tumor EST fragment derived protein #382.
PN DE19820190-A1.
PD 04-NOV-1999.
PA (META-) METAGEN GBS GENOMFORSCHUNG MBH.
Query Match 5.4%; Score 65; DB 2; Length 198;
Best Local Similarity 22.8%; Pred. No. 1.7e+02;

RESULT 1372
ID ABB69252 standard; protein; 200 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34548.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 65; DB 4; Length 200;
Best Local Similarity 27.4%; Pred. No. 1.7e+02;
RESULT 1373
ID ADH42561 standard; protein; 200 AA.
DE Novel human protein NOV78b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 8; Length 200;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
RESULT 1374
ID ADH42563 standard; protein; 200 AA.
DE Novel human protein NOV78c.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 8; Length 200;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
RESULT 1375
ID ADM04770 standard; protein; 221 AA.
DE Human protein of the invention SEQ ID NO:3455.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.4%; Score 65; DB 7; Length 221;
Best Local Similarity 28.2%; Pred. No. 2e+02;
RESULT 1376
ID AAR22754 standard; protein; 233 AA.
DE Reshaped CAMPATH-1 antibody light chain.
PN WO9205274-A.
PD 02-APR-1992.
PA (GORM/) GORMAN S D.
Query Match 5.4%; Score 65; DB 2; Length 233;
Best Local Similarity 21.4%; Pred. No. 2.1e+02;
RESULT 1377
ID AAM24352 standard; protein; 241 AA.
DE Human EST encoded protein SEQ ID NO: 1877.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 241;
Best Local Similarity 24.3%; Pred. No. 2.2e+02;
RESULT 1378
ID ABB68402 standard; protein; 249 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 65; DB 4; Length 249;
Best Local Similarity 21.4%; Pred. No. 2.3e+02;
RESULT 1379
ID ADC39138 standard; protein; 251 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 80.
PN WO200310327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 7; Length 251;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
RESULT 1380
ID ADH42565 standard; protein; 251 AA.
DE Novel human protein NOV78d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 8; Length 251;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
RESULT 1381

ID ADN72615 standard; protein; 264 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 510.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match 5.4%; Score 65; DB 8; Length 264;
Best Local Similarity 26.4%; Pred. No. 2.5e+02;
RESULT 1382
ID ABM74023 standard; protein; 279 AA.
DE DNA clone originating in barley containing SNP sequence #433.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNVI-) UNIV JAPAN OKAYAMA.
Query Match 5.4%; Score 65; DB 7; Length 279;
Best Local Similarity 23.6%; Pred. No. 2.7e+02;
RESULT 1383
ID ADF76971 standard; protein; 290 AA.
DE Novel human secreted and transmembrane protein SeqID 646.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GERTH-) GENENTECH INC.
Query Match 5.4%; Score 65; DB 7; Length 290;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
RESULT 1384
ID ADE58981 standard; protein; 306 AA.
DE Rat Protein Q62632, SEQ ID NO 4869.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 5.4%; Score 65; DB 7; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1385
ID ADE58989 standard; protein; 306 AA.
DE Rat Protein Q62632, SEQ ID NO 4877.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 5.4%; Score 65; DB 7; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1386
ID ADE58993 standard; protein; 306 AA.
DE Rat Protein Q62632, SEQ ID NO 4881.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 5.4%; Score 65; DB 7; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1387
ID ADE58985 standard; protein; 306 AA.
DE Rat Protein Q62632, SEQ ID NO 4873.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 5.4%; Score 65; DB 7; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1388
ID ADF42736 standard; protein; 306 AA.
DE Rat FRP amino acid sequence SEQ ID NO:42.
PN WO2003102163-A2.
PD 11-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 5.4%; Score 65; DB 8; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1389
ID ADO80878 standard; protein; 306 AA.
DE SPARC family protein FRP SEQ ID NO:47.
PN WO2004064785-A2.
PD 05-AUG-2004.
PA (DAND-) DANA FARBER CANCER INST.

Query Match 5.4%; Score 65; DB 8; Length 306;
Best Local Similarity 18.9%; Pred. No. 3.1e+02;
RESULT 1390
ID AHI03102 standard; protein; 320 AA.
DE Thermococcus DNA polymerase JDF-3 mutant 33, fragment.
PN WO200132887-A1.
PD 10-MAY-2001.
PA (STRA-) STRATAGENE.
Query Match 5.4%; Score 65; DB 4; Length 320;
Best Local Similarity 24.2%; Pred. No. 3.2e+02;
RESULT 1391
ID ADS09240 standard; protein; 322 AA.
DE Allotococcus citilis antigenic protein SEQ ID NO:3180.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP-) WYETH HOLDINGS CORP.
Query Match 5.4%; Score 65; DB 6; Length 322;
Best Local Similarity 20.7%; Pred. No. 3.3e+02;
RESULT 1392
ID ABB62686 standard; protein; 324 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14850.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERKE-) PE CORP NY.
Query Match 5.4%; Score 65; DB 4; Length 324;
Best Local Similarity 21.8%; Pred. No. 3.3e+02;
RESULT 1393
ID ADS21636 standard; protein; 336 AA.
DE Bacterial polypeptide #10669.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 65; DB 8; Length 336;
Best Local Similarity 20.7%; Pred. No. 3.3e+02;
RESULT 1394
ID AAM41060 standard; protein; 348 AA.
DE Human polypeptide SEQ ID NO 5991.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 348;
Best Local Similarity 23.6%; Pred. No. 3.6e+02;
RESULT 1395
ID ADE09981 standard; protein; 348 AA.
DE Novel protein-related config polypeptide sequence #569.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 7; Length 348;
Best Local Similarity 23.6%; Pred. No. 3.6e+02;
RESULT 1396
ID ABO66451 standard; protein; 364 AA.
DE Klebsiella pneumoniae polypeptide seqid 12968.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65; DB 7; Length 364;
Best Local Similarity 25.5%; Pred. No. 3.9e+02;
RESULT 1397
ID ABG93295 standard; protein; 406 AA.
DE C. albicans BAX-associated protein Fragment SEQ ID 548.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JUNC-) JANSSEN PHARM NV.
Query Match 5.4%; Score 65; DB 5; Length 406;
Best Local Similarity 20.1%; Pred. No. 4.5e+02;
RESULT 1398
ID ADC39136 standard; protein; 422 AA.
DE Novel human NOVX polypeptide SEQ ID NO: 78.

PN WO2003010327-A2.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 7; Length 422;
Best Local Similarity 33.3%; Pred. No. 4.7e+02;
RESULT 1399
ID ADH42559 standard; protein; 422 AA.
DE Novel human protein NOV78a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 65; DB 8; Length 422;
Best Local Similarity 33.3%; Pred. No. 4.7e+02;
RESULT 1400
ID AAR32085 standard; protein; 427 AA.
DE Benzene dioxygenase polypeptide I.
PN JP05003785-A.
PD 14-JAN-1993.
PA (SAOC) MERCIAN CORP.
Query Match 5.4%; Score 65; DB 2; Length 427;
Best Local Similarity 23.7%; Pred. No. 4.8e+02;
RESULT 1401
ID AAU04136 standard; protein; 430 AA.
DE Tomato REV protein.
PN WO200133944-A1.
PD 17-MAY-2001.
PA (SLAD/) SLADE A.
PA (MADI/) MADISEN L.
PA (COMA/) COMAI L.
Query Match 5.4%; Score 65; DB 4; Length 430;
Best Local Similarity 29.7%; Pred. No. 4.9e+02;
RESULT 1402
ID ABO70247 standard; protein; 445 AA.
DE Pseudomonas aeruginosa polypeptide #2422.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65; DB 7; Length 445;
Best Local Similarity 21.8%; Pred. No. 5.1e+02;
RESULT 1403
ID ABU08678 standard; protein; 449 AA.
DE Novel human thymidylate kinase subfamily kinase.
PN US6489153-B1.
PD 03-DEC-2002.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 65; DB 6; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1404
ID AAB38613 standard; protein; 449 AA.
DE Human thymidylate kinase protein.
PN WO2003064642-A1.
PD 07-AUG-2003.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 65; DB 7; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1405
ID ADC63370 standard; protein; 449 AA.
DE Human novel kinase protein.
PN US2003087294-A1.
PD 08-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 5.4%; Score 65; DB 7; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1406
ID ADI40851 standard; protein; 449 AA.
DE Human kinase and phosphatase KXP-17 protein SEQ ID NO.17.
PN WO2004009778-A2.
PD 29-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.4%; Score 65; DB 8; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1407
ID ADN49356 standard; protein; 449 AA.

DE Human kinase protein.
PN US2004081999-A1.
PD 29-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 5.4%; Score 65; DB 8; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1408
ID ADP84606 standard; protein; 449 AA.
DE Human breast-specific protein #110.
PN WO2004053077-A2.
PD 24-JUN-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 5.4%; Score 65; DB 8; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1409
ID ABW80259 standard; protein; 449 AA.
DE Tumour-associated antigenic target (TAR) polypeptide PRO80771, SEQ.654.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 65; DB 8; Length 449;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
RESULT 1410
ID ABB09145 standard; protein; 454 AA.
DE Human phospholipase A2 protein cPLA2 SEQ ID NO.3.
PN WO20024923-A1.
PD 28-MAR-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 65; DB 5; Length 454;
Best Local Similarity 24.3%; Pred. No. 5.2e+02;
RESULT 1411
ID ADG14228 standard; protein; 454 AA.
DE Partial Human PLA 2 protein.
PN WO2003076935-A1.
PD 18-SEP-2003.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 65; DB 7; Length 454;
Best Local Similarity 24.3%; Pred. No. 5.2e+02;
RESULT 1412
ID ADC51245 standard; protein; 459 AA.
DE ABC cepacia biphenyl dioxygenase, BphA, (LB400) protein.
PN JP2003000269-A.
PD 07-JAN-2003.
PA (KTRI) KIRIN BREWERY KK.
Query Match 5.4%; Score 65; DB 7; Length 459;
Best Local Similarity 25.8%; Pred. No. 5.3e+02;
RESULT 1413
ID AAE25058 standard; protein; 467 AA.
DE Human calpain protein #1.
PN WO200248326-A2.
PD 20-JUN-2002.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 65; DB 5; Length 467;
Best Local Similarity 20.3%; Pred. No. 5.5e+02;
RESULT 1414
ID ADB80781 standard; protein; 470 AA.
DE Microsatellite related FLJ11053 -2 ORF amino acid sequence.
PN WO2003087162-A2.
PD 23-OCT-2003.
PA (MTMM-) MTM LAB AG.
Query Match 5.4%; Score 65; DB 7; Length 470;
Best Local Similarity 17.2%; Pred. No. 5.5e+02;
RESULT 1415
ID ADB80782 standard; protein; 471 AA.
DE Microsatellite related FLJ11053 +1 ORF amino acid sequence.
PN WO2003087162-A2.
PD 23-OCT-2003.
PA (MTMM-) MTM LAB AG.
Query Match 5.4%; Score 65; DB 7; Length 471;
Best Local Similarity 17.2%; Pred. No. 5.5e+02;
RESULT 1416
ID ADB80780 standard; protein; 501 AA.
DE Microsatellite related FLJ11053 -1 ORF amino acid sequence.

PN WO2003087162-A2.
PD 23-OCT-2003.
PA (MTMM-) MTM LAB AG.
Query Match 5.4%; Score 65; DB 7; Length 501;
Best Local Similarity 17.2%; Pred. No. 6e+02;
RESULT 1417
ID ABU3193 standard; protein; 503 AA.
DE Protein encoded by Prokaryotic essential gene #17520.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.4%; Score 65; DB 6; Length 503;
Best Local Similarity 22.9%; Pred. No. 6e+02;
RESULT 1418
ID ADN21340 standard; protein; 510 AA.
DE Bacterial polypeptide #3993.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 65; DB 8; Length 510;
Best Local Similarity 19.8%; Pred. No. 6.2e+02;
RESULT 1419
ID AAB47156 standard; protein; 518 AA.
DE PCNA associated nuclease, PAN.
PN WO200121663-A1.
PD 29-MAR-2001.
PA (RIGE-) RIGEL PHARM INC.
Query Match 5.4%; Score 65; DB 4; Length 518;
Best Local Similarity 21.5%; Pred. No. 6.3e+02;
RESULT 1420
ID ADQ19220 standard; protein; 518 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2039.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.4%; Score 65; DB 8; Length 518;
Best Local Similarity 21.5%; Pred. No. 6.3e+02;
RESULT 1421
ID ADM87191 standard; protein; 530 AA.
DE Human protein SEQ ID NO.284.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NOVE-) NOVELO INC.
Query Match 5.4%; Score 65; DB 8; Length 530;
Best Local Similarity 20.5%; Pred. No. 6.5e+02;
RESULT 1422
ID ABO66883 standard; protein; 574 AA.
DE Klebsiella pneumoniae polypeptide seqid 13400.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.4%; Score 65; DB 7; Length 574;
Best Local Similarity 22.2%; Pred. No. 7.2e+02;
RESULT 1423
ID ADC73072 standard; protein; 590 AA.
DE P chrysoosporium cellulolytic enzyme-related protein - SEQ ID 29.
PN WO2003070940-A1.
PD 28-AUG-2003.
PA (OUIP) OUI PAPER CO.
Query Match 5.4%; Score 65; DB 7; Length 590;
Best Local Similarity 24.0%; Pred. No. 7.5e+02;
RESULT 1424
ID ADRE8697 standard; protein; 597 AA.
DE Human NOV18a protein - SEQ ID 74.
PN WO2003040330-A2.
PD 15-MAY-2003.
PA (CUNA-) CUPAGEN CORP.
Query Match 5.4%; Score 65; DB 7; Length 597;
Best Local Similarity 22.2%; Pred. No. 7.6e+02;

RESULT 1425
ID ADM93442 standard; protein; 597 AA.
DE Human NOVX polypeptide #37.
PN US2004067882-A1.
PD 08-APR-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (BARO/) BARON M.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (DHAN/) DHANABAL M.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (ETTE/) ETTERBERG S.
PA (GANG/) GANGOLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GROS/) GROSSE W M.
PA (GUOX/) GUO X.
PA (HACK/) HACKETT C.
PA (JTWI/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LEPL/) LEPEL D M.
PA (LILU/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MAZU/) MAZUR A.
PA (MCOU/) MCOULENEY K.
PA (MEZE/) MEZES P S.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (MISH/) MISHRA V.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENM/) PENNA C E A.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (STAR/) STARLING G.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TCHE/) TCHERNEY V T.
PA (TWOI/) TWOMLOW N.
PA (VERN/) VERNET C A M.
PA (ZERR/) ZERRHUSEN B D.
PA (VOSS/) VOSS B Z.
PA (ZHON/) ZHONG M.
Query Match 5.4%; Score 65; DB 8; Length 597;
Best Local Similarity 22.2%; Pred. No. 7.6e+02;
RESULT 1426
ID ABM84840 standard; protein; 607 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO.5089.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.4%; Score 65; DB 8; Length 607;
Best Local Similarity 23.2%; Pred. No. 7.8e+02;
RESULT 1427
ID ADD46676 standard; protein; 608 AA.
DE Rat Protein AAC93938, SEQ ID NO 12361.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.
Query Match 5.4%; Score 65; DB 7; Length 608;
Best Local Similarity 22.0%; Pred. No. 7.8e+02;
RESULT 1428
ID ABB91334 standard; protein; 614 AA.
DE Herbicidically active polypeptide SEQ ID NO 545.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 65; DB 5; Length 614;
Best Local Similarity 21.0%; Pred. No. 7.9e+02;
RESULT 1429
ID AAR10795 standard; protein; 622 AA.
DE Human prolactin receptor.
PN US4992378-A.
PD 12-FEB-1991.
PA (ROYA-) ROYAL INSTR ADVAN LE.
Query Match 5.4%; Score 65; DB 2; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1430
ID ABU05555 standard; protein; 622 AA.
DE Breast cancer-associated protein 20.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.4%; Score 65; DB 5; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1431
ID AAU99354 standard; protein; 622 AA.
DE Human prolactin receptor (PRLR) protein.
PN WO200250098-A2.
PD 27-JUN-2002.
PA (GENA-) GENVAISSANCE PHARM INC.
Query Match 5.4%; Score 65; DB 5; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1432
ID AAU99355 standard; protein; 622 AA.
DE Human prolactin receptor (PRLR) variant protein.
PN WO200250098-A2.
PD 27-JUN-2002.
PA (GENA-) GENVAISSANCE PHARM INC.
Query Match 5.4%; Score 65; DB 5; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1433
ID ABR47367 standard; protein; 622 AA.
DE Breast cancer associated protein sequence SEQ ID NO:373.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 5.4%; Score 65; DB 6; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1434
ID ADN99426 standard; protein; 622 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A26.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.4%; Score 65; DB 7; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1435
ID ADN8794 standard; protein; 622 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:112.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.4%; Score 65; DB 7; Length 622;
Best Local Similarity 22.2%; Pred. No. 8.1e+02;
RESULT 1436
ID AAB93459 standard; protein; 630 AA.
DE Human protein sequence SEQ ID NO:12720.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.

Query Match 5.4%; Score 65; DB 4; Length 630;
Best Local Similarity 17.2%; Pred. No. 8.2e+02;
RESULT 1437
ID ADB80779 standard; protein; 630 AA.
DE Microsatellite related FLJ11053 wt ORF amino acid sequence.
PN WO2003087162-A2.
PD 23-OCT-2003.
PA (MTMM-) MTM LAB AG.
Query Match 5.4%; Score 65; DB 7; Length 630;
Best Local Similarity 17.2%; Pred. No. 8.2e+02;
RESULT 1438
ID ABUS2983 standard; protein; 672 AA.
DE Human testes-derived protein from DKFZphes3_15h1.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GERU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.4%; Score 65; DB 4; Length 672;
Best Local Similarity 20.5%; Pred. No. 9e+02;
RESULT 1439
ID ABR05342 standard; protein; 674 AA.
DE Pancreas-originated sodium ion/glucose transporter (SGLT) protein #1.
PN WO200253738-A1.
PD 11-JUL-2002.
PA (TAKEDA) TAKEDA CHEM IND LTD.
Query Match 5.4%; Score 65; DB 5; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1440
ID ABR05347 standard; protein; 674 AA.
DE Pancreas-originated sodium ion/glucose transporter (SGLT) protein #5.
PN WO200253738-A1.
PD 11-JUL-2002.
PA (TAKEDA) TAKEDA CHEM IND LTD.
Query Match 5.4%; Score 65; DB 5; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1441
ID ABR05346 standard; protein; 674 AA.
DE Pancreas-originated sodium ion/glucose transporter (SGLT) protein #4.
PN WO200253738-A1.
PD 11-JUL-2002.
PA (TAKEDA) TAKEDA CHEM IND LTD.
Query Match 5.4%; Score 65; DB 5; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1442
ID AAB36063 standard; protein; 674 AA.
DE Human transporter protein #4.
PN WO2002102986-A2.
PD 27-DEC-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65; DB 6; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1443
ID ADB85297 standard; protein; 674 AA.
DE Human Na-glucose transporter protein.
PN WO2003056005-A1.
PD 10-JUL-2003.
PA (TAKEDA) TAKEDA CHEM IND LTD.
Query Match 5.4%; Score 65; DB 7; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1444
ID ADO09778 standard; protein; 674 AA.
DE Human SGLT homologue protein SEQ ID NO:1.
PN WO2004039405-A1.
PD 13-MAY-2004.
PA (TAKEDA) TAKEDA CHEM IND LTD.
Query Match 5.4%; Score 65; DB 8; Length 674;
Best Local Similarity 23.2%; Pred. No. 9e+02;
RESULT 1445
ID AA014202 standard; protein; 681 AA.
DE Human transporter and ion channel TRICH-19.
PN WO200204520-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65; DB 5; Length 681;

Best Local Similarity 23.2%; Pred. No. 9.2e+02;
RESULT 1446
ID AAE36062 standard; protein; 681 AA.
DE Human transporter protein #3.
PN WO2002102986-A2.
PD 27-DEC-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65; DB 6; Length 681;
Best Local Similarity 23.2%; Pred. No. 9.2e+02;
RESULT 1447
ID ADJ81711 standard; protein; 681 AA.
DE Human SMINT2010324 protein with sugar transportation carrier activity #2.
PN JP2004000177-A.
PD 08-JAN-2004.
PA (KISP) KISSEI YAKUHIN KOGYO KK.
Query Match 5.4%; Score 65; DB 8; Length 681;
Best Local Similarity 23.2%; Pred. No. 9.2e+02;
RESULT 1448
ID AAE05962 standard; protein; 687 AA.
DE Human phospholipase-related protein.
PN WO200153326-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 687;
Best Local Similarity 24.3%; Pred. No. 9.3e+02;
RESULT 1449
ID ADJ70619 standard; protein; 700 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2425.
PN WO2002087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
Query Match 5.4%; Score 65; DB 7; Length 700;
Best Local Similarity 23.4%; Pred. No. 9.5e+02;
RESULT 1450
ID AAE05957 standard; protein; 710 AA.
DE Human phospholipase-like protein #2.
PN WO200153326-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 710;
Best Local Similarity 24.3%; Pred. No. 9.7e+02;
RESULT 1451
ID AAB69719 standard; protein; 720 AA.
DE Human polypeptide SEQ ID NO 1766.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 5; Length 720;
Best Local Similarity 23.2%; Pred. No. 9.9e+02;
RESULT 1452
ID AABM8064 standard; protein; 723 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81219, SEQ.1566.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 65; DB 8; Length 723;
Best Local Similarity 21.4%; Pred. No. 9.9e+02;
RESULT 1453
ID AAY70451 standard; protein; 724 AA.
DE Human membrane channel protein-1 (MECHP-1).
PN WO200012711-A2.
PD 09-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.4%; Score 65; DB 3; Length 724;
Best Local Similarity 24.7%; Pred. No. 1e+03;
RESULT 1454
ID AAE36065 standard; protein; 728 AA.
DE Human transporter protein #6.
PN WO2002102986-A2.
PD 27-DEC-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65; DB 6; Length 728;

Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 1455
ID AAE36064 standard; protein; 745 AA.
DE Human transporter protein #5.
PN WO2002102986-A2.
PD 27-DEC-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 5.4%; Score 65; DB 6; Length 745;
Best Local Similarity 23.2%; Pred. No. 1e+03;
RESULT 1456
ID AABM8155 standard; protein; 752 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82351, SEQ.4015.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 65; DB 8; Length 752;
Best Local Similarity 24.7%; Pred. No. 1e+03;
RESULT 1457
ID ADR90298 standard; protein; 756 AA.
DE Geotrichum sp. M128 xyloglucanendohydrolase mature protein.
PN JP2004261037-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
Query Match 5.4%; Score 65; DB 8; Length 756;
Best Local Similarity 22.7%; Pred. No. 1.1e+03;
RESULT 1458
ID ADR90302 standard; protein; 757 AA.
DE Geotrichum sp. M128 xyloglucanendohydrolase mature protein + Met.
PN JP2004261037-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
Query Match 5.4%; Score 65; DB 8; Length 757;
Best Local Similarity 22.7%; Pred. No. 1.1e+03;
RESULT 1459
ID ADR90296 standard; protein; 776 AA.
DE Geotrichum sp. M128 xyloglucanendohydrolase precursor protein.
PN JP2004261037-A.
PD 24-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
Query Match 5.4%; Score 65; DB 8; Length 776;
Best Local Similarity 22.7%; Pred. No. 1.1e+03;
RESULT 1460
ID AAB43670 standard; protein; 777 AA.
DE Human cancer associated protein sequence SEQ ID NO:1115.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 65; DB 3; Length 777;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 1461
ID ADS10657 standard; protein; 846 AA.
DE Human therapeutic protein - SEQ ID 894.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.4%; Score 65; DB 8; Length 846;
Best Local Similarity 23.4%; Pred. No. 1.2e+03;
RESULT 1462
ID ABB07494 standard; protein; 848 AA.
DE Human lipid metabolism molecule (LMM) polypeptide (ID: 1281946CD1).
PN WO200204490-A2.
PD 17-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.4%; Score 65; DB 5; Length 848;
Best Local Similarity 24.3%; Pred. No. 1.2e+03;
RESULT 1463
ID ABB09144 standard; protein; 849 AA.
DE Human phospholipase A2 protein cPLA2 SEQ ID NO:1.
PN WO200224923-A1.
PD 28-MAR-2002.
PA (KTOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 65; DB 5; Length 849;
Best Local Similarity 24.3%; Pred. No. 1.2e+03;

RESULT 1464
ID ADR08121 standard; protein; 849 AA.
DE Novel protein (useful for identifying genetic disorders) #276.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 7; Length 849;
Best Local Similarity 24.3%; Pred. No. 1.2e+03;
RESULT 1465
ID ADG14226 standard; protein; 849 AA.
DE Human PLA 2 protein.
PN WO2003076935-A1.
PD 18-SEP-2003.
PA (KTOW) KYOWA HAKKO KOGYO KK.
Query Match 5.4%; Score 65; DB 7; Length 849;
Best Local Similarity 24.3%; Pred. No. 1.2e+03;
RESULT 1466
ID ADS10611 standard; protein; 849 AA.
DE Human therapeutic protein - SEQ ID 848.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NIVE-) NIVELO INC.
Query Match 5.4%; Score 65; DB 8; Length 849;
Best Local Similarity 24.3%; Pred. No. 1.2e+03;
RESULT 1467
ID AAM78324 standard; protein; 851 AA.
DE Human protein SEQ ID NO 986.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 851;
Best Local Similarity 23.4%; Pred. No. 1.2e+03;
RESULT 1468
ID AAV00938 standard; protein; 877 AA.
DE M. prunae DNA polymerase 23Pyl protein sequence.
PN WO9907837-A1.
PD 18-FEB-1999.
PA (DIVE-) DIVERSA INC.
Query Match 5.4%; Score 65; DB 2; Length 877;
Best Local Similarity 22.8%; Pred. No. 1.3e+03;
RESULT 1469
ID AAE22115 standard; protein; 877 AA.
DE Metallophera prunae DNA polymerase.
PN WO200220735-A2.
PD 14-MAR-2002.
PA (DIVE-) DIVERSA CORP.
Query Match 5.4%; Score 65; DB 5; Length 877;
Best Local Similarity 22.8%; Pred. No. 1.3e+03;
RESULT 1470
ID ABB50264 standard; protein; 921 AA.
DE DKFZPS60031 ovarian tumour marker protein, SEQ ID NO:16.
PN WO200115177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.4%; Score 65; DB 4; Length 921;
Best Local Similarity 25.9%; Pred. No. 1.4e+03;
RESULT 1471
ID ADP23117 standard; protein; 921 AA.
DE PRO polypeptide SEQ ID NO:211.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 65; DB 8; Length 921;
Best Local Similarity 25.9%; Pred. No. 1.4e+03;
RESULT 1472
ID ABG20052 standard; protein; 947 AA.
DE Novel human diagnostic protein #20043.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 947;
Best Local Similarity 25.9%; Pred. No. 1.4e+03;
RESULT 1473

ID AAM81028 standard; protein; 951 AA.
DE ER interacting domain of AIB1 protein.
PN WO9857982-A2.
PD 23-DEC-1998.
PA (USGO) US GOVERNMENT.
Query Match 5.4%; Score 65; DB 2; Length 951;
Best Local Similarity 19.3%; Pred. No. 1.4e+03;
RESULT 1474
ID ABU03688 standard; protein; 951 AA.
DE Human expressed protein tag (EPT) #354.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 951;
Best Local Similarity 19.3%; Pred. No. 1.4e+03;
RESULT 1475
ID AAY70775 standard; protein; 983 AA.
DE Follistatin-related protein zfstaz.
PN WO200022126-A1.
PD 20-APR-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 65; DB 3; Length 983;
Best Local Similarity 23.4%; Pred. No. 1.5e+03;
RESULT 1476
ID AAE22858 standard; protein; 983 AA.
DE Human zfstaz protein.
PN US6355788-B1.
PD 12-MAR-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 5.4%; Score 65; DB 5; Length 983;
Best Local Similarity 23.4%; Pred. No. 1.5e+03;
RESULT 1477
ID ABU62108 standard; protein; 983 AA.
DE Human follistatin related protein zfstaz.
PN US2003023067-A1.
PD 30-JAN-2003.
PA (CONK/) CONKLIN D C.
PA (ELLS/) ELLSWORTH J L.
Query Match 5.4%; Score 65; DB 6; Length 983;
Best Local Similarity 23.4%; Pred. No. 1.5e+03;
RESULT 1478
ID ABG20044 standard; protein; 987 AA.
DE Novel human diagnostic protein #20035.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 987;
Best Local Similarity 25.9%; Pred. No. 1.5e+03;
RESULT 1479
ID AAU27769 standard; protein; 990 AA.
DE Human full-length polypeptide sequence #94.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 990;
Best Local Similarity 25.9%; Pred. No. 1.5e+03;
RESULT 1480
ID ADS24143 standard; protein; 1100 AA.
DE Bacterial polypeptide #13176.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.4%; Score 65; DB 8; Length 1100;
Best Local Similarity 23.0%; Pred. No. 1.8e+03;
RESULT 1481
ID AAM39633 standard; protein; 1117 AA.
DE Human polypeptide SEQ ID NO 2778.
PN WO200153312-A1.
PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1117;
Best Local Similarity 25.9%; Pred. No. 1.8e+03;
RESULT 1483
ID AB084453 standard; protein; 1157 AA.
DE Mouse cancer-associated protein MP13-011.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.4%; Score 65; DB 8; Length 1157;
Best Local Similarity 20.1%; Pred. No. 1.9e+03;
RESULT 1483
ID AA029529 standard; protein; 1158 AA.
DE Novel human secreted protein #20.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1158;
Best Local Similarity 25.2%; Pred. No. 1.9e+03;
RESULT 1484
ID AA039631 standard; protein; 1192 AA.
DE Human polypeptide SEQ ID NO 2776.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1192;
Best Local Similarity 25.9%; Pred. No. 2e+03;
RESULT 1485
ID AA041419 standard; protein; 1225 AA.
DE Human polypeptide SEQ ID NO 6350.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1225;
Best Local Similarity 25.9%; Pred. No. 2e+03;
RESULT 1486
ID AA041418 standard; protein; 1225 AA.
DE Human polypeptide SEQ ID NO 6349.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1225;
Best Local Similarity 25.9%; Pred. No. 2e+03;
RESULT 1487
ID AA041417 standard; protein; 1225 AA.
DE Human polypeptide SEQ ID NO 6348.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 4; Length 1225;
Best Local Similarity 25.9%; Pred. No. 2e+03;
RESULT 1488
ID ADB82702 standard; protein; 1261 AA.
DE Human protein sequence useful for the treatment of cancer (SeqID 1483).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 7; Length 1261;
Best Local Similarity 25.9%; Pred. No. 2.1e+03;
RESULT 1489
ID AAG38592 standard; protein; 1291 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47633.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 3; Length 1291;
Best Local Similarity 26.4%; Pred. No. 2.2e+03;
RESULT 1490
ID AA047157 standard; protein; 1296 AA.
DE Nevold basal cell carcinoma syndrome (NBCCS) (PTC) protein.
PN WO974314-A2.
PD 20-NOV-1997.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query Match 5.4%; Score 65; DB 2; Length 1296;
Best Local Similarity 22.0%; Pred. No. 2.2e+03;
RESULT 1491
ID ADM67208 standard; protein; 1343 AA.
DE Murine adipocyte specific leukocyte common antigen protein SeqID 562.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Query Match 5.4%; Score 65; DB 8; Length 1343;
Best Local Similarity 20.1%; Pred. No. 2.3e+03;
RESULT 1492
ID AAG38591 standard; protein; 1371 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47632.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 65; DB 3; Length 1371;
Best Local Similarity 26.4%; Pred. No. 2.4e+03;
RESULT 1493
ID AAB59278 standard; protein; 1412 AA.
DE Human SRC-3 protein.
PN US6156571-A.
PD 05-DEC-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 5.4%; Score 65; DB 4; Length 1412;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1494
ID AB003690 standard; protein; 1412 AA.
DE Human expressed protein tag (EPT) #356.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1412;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1495
ID AB003685 standard; protein; 1412 AA.
DE Human expressed protein tag (EPT) #351.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1412;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1496
ID AB003686 standard; protein; 1412 AA.
DE Human expressed protein tag (EPT) #352.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1412;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1497
ID AB003691 standard; protein; 1412 AA.
DE Human expressed protein tag (EPT) #357.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1412;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1498
ID AD070476 standard; protein; 1415 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2282.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.4%; Score 65; DB 7; Length 1415;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1499
ID AB003693 standard; protein; 1417 AA.
DE Human expressed protein tag (EPT) #359.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1417;

Best Local Similarity 19.3%; Pred. No. 2.5e+03;
RESULT 1500
ID ABU03682 standard; protein; 1417 AA.
DE Human expressed protein tag (EPT) #348.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 5.4%; Score 65; DB 6; Length 1417;
Best Local Similarity 19.3%; Pred. No. 2.5e+03;
